

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: June 9, 2004, 18:10:48 ; Search time 19489 seconds

(without alignments)
7078.910 Million cell updates/sec

Title: US-10-072-077A-1

Sequence: 1 gatattcttttattatca.....tatcttactagatcgaattc 3183

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenBml:*

1: gb_ba:*

2: gb_bhg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_par:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_ov:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_in:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rtd:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	3183	100.0	3183 6	175096
2	3171	99.6	3182 6	AR201516
3	2182.4	68.6	3182 8	ATU37336
4	2075.8	65.2	59648 8	AB016870
5	733.4	23.0	1236 1	TIPTMR
6	733.4	23.0	1988 1	ATTMR
7	733.4	23.0	24595 1	ATACH5
8	733.4	23.0	24595 6	E00404
9	733.4	23.0	24595 6	E00546
10	733.4	23.0	24595 6	AR364803
11	733.4	23.0	24595 6	BD016312
12	733.4	23.0	194140 1	AF242881
13	709	22.3	709 6	175097
14	709	22.3	709 6	AR201517
15	636.6	20.0	1983 1	ATTMRPT
16	636.6	20.0	206479 1	AB016260
17	635	19.9	9331 1	AB007927
18	635	19.9	10377 1	AE009419
19	633.4	19.9	29524 1	ATU237588
20	630.2	19.8	1997 1	AB025109
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24	614.4	19.3	14960 1	AVU83986
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ALIGNMENTS

RESULT 1

LOCUS 175096

DEFINITION Sequence 1 from patent US 5689042.

ACCESSION 175096

VERSION 175096.1 GI:3011237

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3183)

AUTHORS Aasino,R.M. and Gan,S.

TITLE Transgenic plants with altered senescence characteristics

JOURNAL Patent: US 5689042-A 1 18-NOV-1997;

FEATURES Location/Qualifiers

DNA linear PAT 03-APR-1998

Source 1. 3183
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 100.0%; Score 3183; DB 6; Length 3183;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GAAATCTCTTTTATATCAACAATAAGTAGTGAAGATGTTGGAAGAGACACTATT 60
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DB 61 CTCGTGAGCACCCAGCTCTGTTTATATTTAGAAACCCGATGTTATTTTGAAGAC 120
QY 121 AAAAAAGTAAATGCTGATGTTTAAATTTAAATTTAGTTTCATCAAGTTTGCATAAA 180
DB 121 AAAAAAGTAAATGCTGATGTTTAAATTTAAATTTAGTTTCATCAAGTTTGCATAAA 180
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DB 241 TTTTCTCTCTTGGTCTTTCTTAACATTAAGAAACCCATTAACAATGTAAGTTCAAT 300
QY 301 AATTAAACAAATATTTCCAAAGTTTATATACGAACCTGTTTATTAATGAACAGTT 360
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QY 421 ATGAATCTAGTGTATATACAAAGAAATGAATGCTATTTAAATACCATCATGAAGTT 480
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QY 1321 GGGAAACATCATGTAACAGAAACTTTTACCAATCATATCATGATTTACTCAAAAGAT 1380
DB 1321 GGGAAACATCATGTAACAGAAACTTTTACCAATCATATCATGATTTACTCAAAAGAT 1380
QY 1381 ACTTACCTAATGAAGTGTACCTGTTGTAATGACATGATTTGATTTGATTTTATTT 1440
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QY 1441 TTGTGAAATCAATTTTCTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1500
DB 1441 TTGTGAAATCAATTTTCTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1500
QY 1501 TGTGAAATTAACGAATCTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1560
DB 1501 TGTGAAATTAACGAATCTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1560
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QY 1621 AAATTAACATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1680
DB 1621 AAATTAACATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1680
QY 1681 TACATGATGATTTTATTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1740
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QY 1801 TCGAAATCTCTATATGACAGATGAGAAATTAATTTTACTATGATCAAACTTCTTA 1860
DB 1801 TCGAAATCTCTATATGACAGATGAGAAATTAATTTTACTATGATCAAACTTCTTA 1860
QY 1861 ATCATCAATTTAATATGTTTAAAGAAATTAATTTTAAACCCACATTAATTTAAAT 1920
DB 1861 ATCATCAATTTAATATGTTTAAAGAAATTAATTTTAAACCCACATTAATTTAAAT 1920
QY 1921 CCGAGCAAAAGTGAAGCAAGCTTATTTGATTTGATTTGATTTGATTTGATTTGATTT 1980
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QY 1981 TATCAACATCAAGATCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2040
DB 1981 TATCAACATCAAGATCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2040
QY 2041 AAAAACTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2100

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QY 2881 GGTCAATCCGTTCCGAAAGTATTAGTTAGTACGCGACCGCTGAGCTGATCGTCAACATTT 2940
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QY 2941 GGCATTAAGTTCTTAAAGTTAGTAACTCTGTGCGCGCTTTCGAGATTAATCAATTAAT 3000
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Db 3120 TATGCGCGCAACCTGGATTAATTAATGCGCGCGGTGATGATGTTATGATCGAA 3179
QY 3181 TTC 3183
Db 3180 TTC 3182

RESULT 3

ATU37336

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

SOURCE

MEDLINE

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 Db 1081 AATCATTAATTTTGAATATGAGTATTTGTCAATTTTGAATTTAGATTTTGAAGCG 1140
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 QY 1321 GGGAAACATCATTTGAAACAGAACTTTTGAACAAATGATTTATCTACAAAGAT 1380
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 Db 1921 CCGAGCAAACTGATGACAGAACTTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1980
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Db 1981 TATCAAAATCAACGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2040
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 Db 2161 CATTTACTTCTCTTAACCAATGG 2184

RESULT 4
 LOCUS AB016870
 DEFINITION Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K15122.
 ACCESSION AB016870
 VERSION AB016870.1 GI:3449311
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 1 (sites)
 Asamizu,E., Sato,S., Kaneko,T., Nakamura,Y., Kotani,H., Miyajima,N.
 and Tabata,S.

TITLE Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
 JOURNAL Sequence features of the regions of 1,081,958 bp covered by
 MEDLINE seveneen physically assigned P1 and TAC clones
 PUBMED DNA Res. 5 (6), 379-391 (1998)
 99156233
 10048488
 2 (bases 1 to 59648)
 AUTHORS Nakamura,Y.
 DIRECT SUBMISSION
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 Tel:81-438-52-3935, Fax:81-438-52-3934)
 COMMENT Address for correspondence: kaos@kazusa.or.jp
 For the latest information on annotation of this clone, please see
 http://www.kazusa.or.jp/kaos/cgi-bin/sgd_graph.cgi?c=K15122
 Genes with similarity to proteins in the databases are described in
 'product' or 'note' qualifiers. Genes that have no significant
 protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: Grail
 (Informatics Group, Oak Ridge National Laboratory,
 http://compbio.ornl.gov/grail-1.3/),
 GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
 NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
 Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
 SplicePredictor (Volker Brendel, Stanford University,
 http://gremiin.zool.iastate.edu/cgi-bin/sp.cgi).
 Genes encoding tRNAs are predicted by tRNAscan-SE
 (Sean Eddy, Washington University School of Medicine, St. Louis,
 http://genome.wustl.edu/eddy/tRNAscan-SE/).
 This sequence may not be the entire insert of this clone. It may be
 shorter because we remove overlaps between neighboring submissions.
 The 5' clone is M919 and the 3' clone is M919.

FEATURES

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Query Match 65.2%; Score 2075.8; DB 8; Length 59648;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2166; Conservative 0; Mismatches 17; Indels 10; Gaps 7;

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RESULT 5
LOCUS TIPKR 1296 bp DNA linear BCT 13-MAR-1996
DEFINITION Ti plasmid (from A.tumefaciens octopine strain) tumor morphology gene (tmr).
ACCESSION K02000 GI:154744
VERSION K02000.1
KEYWORDS tmr gene; tumor morphology gene.
SOURCE Plasmid Ti
ORGANISM Plasmid Ti
REFERENCE 1 (bases 1 to 1296)
Lichtenstein, C., Klee, H., Montoya, A., Garfinkel, D., Fuller, S., Flores, C., Neeter, E. and Gordon, M.
Nucleotide sequence and transcript mapping of the tmr gene of the pTiA6NC octopine Ti-plasmid: a bacterial gene involved in plant tumorigenesis
J. Mol. Appl. Genet. 2 (4), 354-362 (1984)
JOURNAL MEDLINE 84241512
PUBMED 6330262
COMMENT Original source text: Plasmid Ti (clone: pTiA6NC.) DNA.
The T-DNA of pTiA6NC encodes eight polyadenylated transcripts (see sites table), and includes at least four genes: tms - tmr - tml - ocs.

FEATURES
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ORIGIN 505 bp upstream of BamHI site.

Query Match 23.0%; Score 733.4; DB 1; Length 1296;
Best Local Similarity 96.0%; Pred. No. 3.1e-106;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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QY 2259 GCTTCAGCTCTTGGCTTGAATCGGGTCAATCGTCTCAATCAATCAACCGGAAGGG 2318
Db 291 GCTTCAGCTCTTGGCTTGAATCGGGTCAATCGTCTCAATCAATCAACCGGAAGGG 350
QY 2319 ACGACCAACAGTGAAGAGTGAAGAGACGCGTCTTACCTTGATGATCGGCTCT 2378
Db 351 ACGACCAACAGTGAAGAGTGAAGAGACGCGTCTTACCTTGATGATCGGCTCT 410
QY 2379 GGTGAGGGTATCATCGCAGCCAGCAAGCTCATCATAGGCTGATCGAGAGGTATPA 2438
Db 411 GGTGAGGGTATCATCGCAGCCAGCAAGCTCATCATAGGCTGATCGAGAGGTATPA 470
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Db 951 GCG 953

RESULT 6
ATTMR 1988 bp DNA linear BCT 12-SEP-1993
LOCUS Agrobacterium tumefaciens tmr-gene encoded by the octopine Ti plasmid (tumor inducing).
DEFINITION
ACCESSION X00010 GI:39172
VERSION X00010.1
KEYWORDS octopine synthetase; plasmid
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens; Alpha proteobacteria; Rhizobiales; Bacteria; Proteobacteria; Agrobacterium group; Agrobacterium.

REFERENCE 1 (bases 1 to 1988)
 AUTHORS Heidekamp, F., Dirkse, W. G., Hille, J. and van Ormondt, H.
 TITLE Nucleotide sequence of the *Agrobacterium tumefaciens* octopine Ti
 plasmid-encoded tmr gene
 JOURNAL Nucleic Acids Res. 11 (1983), 6211-6223 (1983)
 MEDLINE 84015366
 PUBMED 6312414

COMMENT The product of the tmr-gene inhibits root formation of the tumors
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 cytokinin-independent growth of transformed cells.
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ORIGIN
 Query Match 23.0%; Score 733.4; DB 1; Length 1988;
 Best Local Similarity 96.0%; Pred. No. 2.9e-106;
 Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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 2319 ACGACCAACAGTGAAGAACTGAAGGAACGACGCGCTCTACCTTGATGATCGGCTCT 2378
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 DB 1307 CGCTCAGAGATATTTCTATTCATGCGGCCCAACAGAAACAGAAATTCCTCCCAAGTTAC 1366
 QY 2859 AGCGCTTTGAGAGATTCGAGAGTCCGCTTGGATGATGATGATGATGATGATGATGATGAT 2918
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 QY 2919 GAG 2921
 DB 1427 GCG 1429

RESULT 7
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 ACCESSION X00493 J05108 X00282
 VERSION X00493 J05108 X00282
 KEYWORDS octopine synthetase; plasmid; synthetase; terminal repeat;
 unidentified reading frame.
 SOURCE *Agrobacterium tumefaciens* (Rhizobium radiobacter)
 ORGANISM *Agrobacterium tumefaciens*
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 Rhizobiaceae; Rhizobium/Agrobacterium group; *Agrobacterium*.
 REFERENCE 1 (bases 1 to 24595)
 AUTHORS Barker, R. F., Idler, K. B., Thompson, D. V. and Kemp, J. D.
 TITLE Nucleotide sequence of the T-DNA region from the *Agrobacterium*
 tumefaciens octopine Ti plasmid pTi15955
 JOURNAL Plant Mol. Biol. 2, 335-350 (1983)
 REFERENCE 2 (bases 602 to 14237)
 AUTHORS Gielen, J., De Beuckeleer, M., Seurinck, J., Deboeck, F., De Greve, H.,
 Lemmers, M., Van Montagu, M. and Schell, J.
 TITLE The complete nucleotide sequence of the Ti-DNA of the *Agrobacterium*
 tumefaciens plasmid pTiAch5
 JOURNAL EMBO J. 3 (4), 835-846 (1984)
 REFERENCE 3 (bases 1 to 24595)
 AUTHORS Turk, S. C., Nester, E. W. and Hooykaas, P. J.
 TITLE The *vira* promoter is a host-range determinant in *Agrobacterium*
 tumefaciens
 JOURNAL Mol. Microbiol. 7 (5), 719-724 (1992)
 REFERENCE 4 (bases 1 to 24595)
 AUTHORS Guevara-garcia, A., Mosqueda-Cano, G., Arguello-Astorga, G.,
 Simpson, J. and Herrera-Estrrella, L.
 TITLE Tissue-specific and wound-inducible pattern of expression of the
 mannopine synthase promoter is determined by the interaction
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 JOURNAL Plant J. 4 (3), 495-505 (1993)
 MEDLINE 94035196
 PUBMED 8220492

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Query Match 23.0%; Score 733.4; DB 1; Length 24595;
Best Local Similarity 96.0%; Pred. No. 2.1e-106;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

2139 TAATCAATTAAGCAAAAGCTATTACTTTCTTAACCAATGACCTGCACTTAAT 2198
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LOCUS

DEFINITION T1 plasmid T-DNA region.

ACCESSION E00404
VERSION E00404.1 GI:2168687
KEYWORDS JP 198515633-A/1.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria: Proteobacteria: Alphaproteobacteria: Rhizobiales:
Rhizobiaceae: Rhizobium/Agrobacterium group; Agrobacterium.

REFERENCE 1 (bases 1 to 24595)
AUTHORS Garil, E.D., Denitsu, D.S. and Richiyado, E.B.
TITLE SELECTION USING OPINE SYNTHASE GENE
JOURNAL Patent: JP 198515633-A 1 16-AUG-1985;
AGRIJENETIKUS RES ASSOC LTD

COMMENT OS Agrobacterium tumefaciens
PN JP 198515633-A/1
PD 16-AUG-1985
PE 14-SEP-1984 JP 1984193841
PR 14-SEP-1983 US 83 532280
PI GARIL DE DABUR SATSUTON,
PI RICHIIYADO ERU BEIKKA
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FEATURES
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ORIGIN

Query Match 23.0%; Score 733.4; DB 6; Length 24595;
Best Local Similarity 96.0%; Pred. No. 2.1e-106;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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LOCUS	AR364803	24595 bp	DNA	linear	PAT 03-SEP-2003
DEFINITION	Sequence 1 from patent US 5428147.				
ACCESSION	AR364803				
VERSION	AR364803.1	GI:34427834			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 24595)				
AUTHORS	Barker, R. F. and Kemp, J. D.				
TITLE	Octopine T-DNA Promoters				
JOURNAL	Patent: US 5428147-A 1 27-JUN-1995;				
FEATURES	Location/Qualifiers				
source	1..24595				
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Best Local Similarity	96.0%;	Pred. No. 2.1e-106;			
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Qy	2139	TAATCAATTAAAGCAAAAGCTCATTTACTTTCCTAAACCATGAGACCTCGCATTAAT	2198		
Db	8728	TAATATAAAATCATGTTTGTATCAATATACGCAAAAACCTTATGACCTGCACTTAAT	8787		
Qy	2199	TTTGGGTCCAACTTGCAAGAAAGACGACGACCGCATAGCTCTTGGCCAGACAGAG	2258		
Db	8788	TTTGGGTCCAACTTGCAAGAAAGACGACGACCGCGATAGCTCTTGGCCAGACAGAG	8847		
Qy	2259	GCTTCCAGTCCCTTTCGCTTGATCGGGTCCAAATCGTCTCTCAACTATCAACCGGAAGCG	2318		
Db	8848	GCTTCCAGTCCCTTTCGCTTGATCGGGTCCAAATCGTCTCTCAACTATCAACCGGAAGCG	8907		
Qy	2319	ACGACCAACAGTGAAGAACTGAAAGAAAGACGACGCGCTCTAACCCTGATTCGGCTCT	2378		
Db	8908	ACGACCAACAGTGAAGAACTGAAAGAAAGACGCGCTCTAACCCTGATTCGGCTCT	8966		
Qy	2379	GGTGAGGGGTATCATCGACGACCAAGCTCATATAGGCTGATCGAGAGGTGTATTA	2438		
Db	8968	GGTGAAGGGTATCATCGACGACCAAGCTCATATAGGCTGATCGAGAGGTGTATTA	9027		
Qy	2439	TCATGAGGCCAACGGCGGGCTTATCTTGAAGGAGGATCCACTCGTGTCTCAACTGCAT	2498		
Db	9028	TCATGAGGCCAACGGCGGGCTTATCTTGAAGGAGGATCCACTCGTGTCTCAACTGCAT	9087		
Qy	2499	GGCGGGAACACGCTATTTGAGTGCAGATTTTGGTGGCATATTATTTCGCCACAACTTAC	2558		
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Db	9208	TGCAGGCCCATTCCTATTATCAAGAGTGTGTTTATCTTTGAATGCAACTCGGCTGAGGC	9267		
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Db	9328	CACGGAGATATGCTATTCGACTTGAAGCAAAATATGAAAGTAAAGTTGATTAATGGAT	9387		
Qy	2799	CGCTCAGAGATATTTTCATCATGCGCGCCCAACAGAAATTCGCCAAATTAAAGC	2858		
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Db	9448	AGCGCTTCGACAGGANTGGAAAGTCAATCCGTTGCGGAAGTAAATAGTAAAGCTTAACGCGACGCCCT	9507
QY	2919	GAG 2921	
Db	9508	GCG 9510	
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LOCUS			
DEFINITION	BD016312	24595 bp	DNA
			linear
			PAT 27-AUG-2002
			Method of promoting plant transcripction by using octopline T-DNA
ACCESSION	BD016312		
VERSION	BD016312.1	GI:22557450	
KEYWORDS	JP 2001190289-A/1.		
SOURCE	Agrobacterium tumefaciens (Rhizobium radiobacter)		
ORGANISM	Agrobacterium tumefaciens		
	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;		
	Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.		
REFERENCE	1 (bases 1 to 24595)		
AUTHORS	Barke,R.F. and Kemp,J.D.		
TITLE	Method of promoting plant transcripction by using octopline T-DNA		
JOURNAL	Patent: JP 2001190289-A 1 17-JUL-2001;		
	MYCOGEN PLANT SCIENCE INC		
COMMENT	OS Agrobacterium tumefaciens		
	PN JP 2001190289-A/1		
	PD 17-JUL-2001		
	PF 22-NOV-2000 JP 2000356816		
	PR 18-NOV-1983 US 553786		
	PI RICHARD F BARKER,JOHN D KEMP		
	PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC		Method of
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	DNA promoter		
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ORIGIN			
Query Match	23.0%;	Score 733.4;	DB 6;
Best Local Similarity	96.0%;	Prod. No. 2.1e-106;	
Matches 752;	Conservative	0; Mismatches 31;	Indels 0; Gaps 0;
QY	2139	TATCAATTAATAGACAAAGTCAATTAACCTTAAACCATGAGACCTGCATCTAAT	2198
Db	8728	TAAATATAAAATCACTTGTATTCATTAATCTGAAAAAATTATGACCTGCATCTAAT	8787
QY	2199	TTTGGGTCCAACTTGACAGAGAAAGACGACGACCGCATAGCTCTTGCCGACGACACGG	2255
Db	8788	TTTGCGTCCAACTTGACAGAGAAAGACGACGACCGCATAGCTCTTGCCGACGACACGG	8847
QY	2259	GCTTCACATCCCTTCGCTTGAATCGGGTCCCATCGGTCCCACTATCAACCGGAAGCGG	2318
Db	8848	GCTTCACATCCCTTCGCTTGAATCGGGTCCCATCGGTCCCACTATCAACCGGAAGCGG	8907
QY	2319	ACGACCAACAGTGAAGAACTGAAAGGAACAGACGCGTCTCTACCTTGATGATCGGCTCT	2378
Db	8908	ACGACCAACAGTGAAGAACTGAAAGGAACAGACGCGTCTCTACCTTGATGATCGGCTCT	8967
QY	2379	GGTGAGGGTATCATGCGACCAAGCAAGCTCATATAGGCTGATCCAGAGAGTCTATAA	2433
Db	8968	GGTGAGGGTATCATGCGACCAAGCAAGCTCATATAGGCTGATCCAGAGAGTCTATAA	9022
QY	2439	TCATAGGCCCAACGCGCGGGCTTATCTTGAGGAGAGATCCACCTGTTGCTCAACTGCAT	2498
Db	9028	TCATAGGCCCAACGCGCGGGCTTATCTTGAGGAGAGATCCACCTGTTGCTCAACTGCAT	9087
QY	2499	GCGCGAAAACAGCTATTGAGATGACAGATTTTTCGTTGGCATATTAATTCGCCCAAGTTACC	2555

Db 9088 GGGCCGAACAGCTATTGAGTGCAGATTTTCGTTGGCATATTATTGGCCCAAGTTACC 9147

QY 2559 CGACCAAGAGACCTTCATGAAAAGCGCCAAAGCCAGATTAAAGCATGTTGCACCCCGC 2618

Db 9148 CGACCAAGAGACCTTCATGAAAAGCGCCAAAGCCAGATTAAAGCATGTTGCACCCCGC 9207

QY 2619 TGCAGGCGCATTTCTATTATTCAGAGTTGGTTTATCTTTGGAAATTAACCTGGCGTAGAGCC 2678

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QY 2679 CATTCCTAAAGAGATCGCATGATATGCAATATGCAATGTTGTTGGCTAGCCAGAACCATGAT 2738

Db 9268 CATTCCTAAAGAGATCGCATGATATGCAATATGCAATGTTGTTGGCTAGCCAGAACCATGAT 9327

QY 2739 CACGGCAGATATGCTATTATGACGTTGACGCAATATGCAATATGCAATATGCAATATGCAAT 2798

Db 9328 CACGGCAGATATGCTATTATGACGTTGACGCAATATGCAATATGCAATATGCAATATGCAAT 9387

QY 2799 CGCTCAGAGATTTTCATTCATTCGCGGCGCAACAGAAACGAATTCGCCCAAGTTAAGCG 2958

Db 9388 CGCTCAGAGATTTTCATTCATTCGCGGCGCAACAGAAACGAATTCGCCCAAGTTAAGCG 9447

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QY 2919 GAG 2921

Db 9508 GCG 9510

RESULT 12

AF242881 194140 bp DNA circular BCT 26-JUN-2000

LOCUS AF242881

DEFINITION Agrobacterium tumefaciens octopine-type Ti plasmid, complete sequence.

ACCESSION AF242881 AF034854 AF035413 AF035773 AF039887 AF039888 AF117204 AH006976 M14460 M14762 M80605 M80607 U19620 U43674 U43675 U48718 U60011 X04784

VERSION AF242881.1 GI:8572673

KEYWORDS Agrobacterium tumefaciens (Rhizobium radiobacter)

SOURCE ORGANISM

Agrobacterium tumefaciens

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

REFERENCE 1 (bases 193234 to 194140), 1 to 23692)

Barker, R.F., Idler, K.B., Thompson, D.V. and Kemp, J.D.

Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octopine Ti plasmid PT15955

Plant Mol. Biol. 2, 335-350 (1983)

REFERENCE 2 (bases 166443 to 168193)

Yanofsky, M.F. and Nester, E.W.

Molecular characterization of a host-range-determining locus from Agrobacterium tumefaciens

J. Bacteriol. 168 (1), 244-250 (1986)

JOURNAL MEDLINE 87008387

PUBMED 3759904

3 (bases 168089 to 173951)

Yanofsky, M.F., Porter, S.G., Young, C., Albright, L.M., Gordon, M.P. and Nester, E.W.

The virD operon of Agrobacterium tumefaciens encodes a site-specific endonuclease

Cell 47 (3), 471-477 (1986)

JOURNAL MEDLINE 87028239

PUBMED 3021341

4 (bases 175278 to 177719)

Winans, S.C., Allenza, P., Stachel, S.E., McBride, K.E. and Nester, E.W.

Characterization of the virE operon of the Agrobacterium Ti plasmid PT1A6

Nucleic Acids Res. 15 (2), 825-837 (1987)

JOURNAL MEDLINE 87146396

PUBMED 3547330

REFERENCE 5 (bases 50125 to 54471)

Habeeb, I.F., Wang, L. and Winans, S.C.

Transcription of the octopine catabolism operon of the Agrobacterium tumor-inducing plasmid PT1A6 is activated by a LysR-type regulatory protein

Mol. Plant Microbe Interact. 4 (4), 379-385 (1991)

JOURNAL MEDLINE 92190631

PUBMED 1799699

6 (bases 50125 to 54471)

Valdivia, R.H., Wang, L. and Winans, S.C.

Characterization of a putative periplasmic transport system for octopine accumulation encoded by Agrobacterium tumefaciens Ti plasmid PT1A6

J. Bacteriol. 173 (20), 6398-6405 (1991)

JOURNAL MEDLINE 92011411

PUBMED 1657707

7 (bases 68024 to 76460)

Kim, K.S. and Farrand, S.K.

Ti plasmid-encoded genes responsible for catabolism of the crown gall opine mannopine by Agrobacterium tumefaciens are homologs of the T-region genes responsible for synthesis of this opine by the plant tumor

J. Bacteriol. 178 (11), 3275-3284 (1996)

JOURNAL MEDLINE 96236046

PUBMED 8555509

8 (bases 39157 to 45466)

Fuqua, C. and Winans, S.C.

Localization of OccR-activated and Trar-activated promoters that express two ABC-type permeases and the trar gene of Ti plasmid PT1R10

Mol. Microbiol. 20 (6), 1199-1210 (1996)

JOURNAL MEDLINE 96405643

PUBMED 8809772

9 (bases 22855 to 39243; 96353 to 111409)

Alt-Morbe, J., Stryker, J.L., Fuqua, C., Li, P.L., Farrand, S.K. and Winans, S.C.

The conjugal transfer system of Agrobacterium tumefaciens octopine-type Ti plasmids is closely related to the transfer system of an IncP plasmid and distantly related to Ti plasmid vir genes

J. Bacteriol. 178 (14), 4248-4257 (1996)

JOURNAL MEDLINE 96312368

PUBMED 8763954

10 (bases 54312 to 62806)

Oger, P., Kim, K.S., Sackert, R.L., Piper, K.R. and Farrand, S.K.

Octopine-type Ti plasmids code for a mannopine-inducible dominant-negative allele of trar, the quorum-sensing activator that regulates Ti plasmid conjugal transfer

Mol. Microbiol. 27 (2), 277-288 (1998)

JOURNAL MEDLINE 98143415

PUBMED 9484884

11 (bases 133963 to 138972)

Kalogeraki, V.S. and Winans, S.C.

Wound-released chemical signals may elicit multiple responses from an Agrobacterium tumefaciens strain containing an octopine-type Ti plasmid

J. Bacteriol. 180 (21), 5660-5667 (1998)

JOURNAL MEDLINE 99009000

PUBMED 9791116

12 (bases 76455 to 98723)

Ly, S.M., Jafri, S. and Winans, S.C.

Mannopine acid and agropinic acid catabolism region of the octopine-type Ti plasmid PT15955

Mol. Microbiol. 31 (1), 339-347 (1999)

JOURNAL MEDLINE 99141607

PUBMED 9987134

13 (bases 1 to 194140)

Winans, S.C., Zhu, J., Oger, P.M., Schrammeyer, B., Hooykaas, P.J. and Farrand, S.K.

Octopine-type Ti plasmid sequence

Unpublished

REFERENCE 14 (bases 68024 to 76460)

Kim, K.-S.

Direct Submission

JOURNAL Submitted (10-JAN-1995) Kun-Soo Kim, Microbiology, University of Illinois at Urbana-Champaign, 1201 W. Gregory Dr., Urbana, IL 61801, USA

REFERENCE 15 (bases 96353 to 111409)

AUTHORS Winans, S.C.

TITLE Direct Submission

JOURNAL Submitted (20-DEC-1995) Stephen C. Winans, Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

REFERENCE 16 (bases 39167 to 45466)

AUTHORS Fugua, C.

TITLE Direct Submission

JOURNAL Submitted (07-FEB-1996) Clay Fugua, Biology, Trinity University, 715 Stadium Dr., San Antonio, TX 78212, USA

REFERENCE 17 (bases 54312 to 62806)

AUTHORS Kim, K.-S., Sackett, R.L., and Farrand, S.K.

TITLE Direct Submission

JOURNAL Submitted (04-JUN-1996) Crop Sciences, University of Illinois at Urbana-Champaign, 240 ERML, 1201 W. Gregory Dr., Urbana, IL 61801, USA

REFERENCE 18 (bases 186239 to 193239)

AUTHORS Zhu, J., and Winans, S.C.

TITLE Direct Submission

JOURNAL Submitted (17-NOV-1997) Section of Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

REFERENCE 19 (bases 76455 to 98723)

AUTHORS Winans, S.C., and Ly, S.

TITLE Direct Submission

JOURNAL Submitted (20-NOV-1997) Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

REFERENCE 20 (bases 170209 to 175283)

AUTHORS Zhu, J., and Winans, S.C.

TITLE Direct Submission

JOURNAL Submitted (25-NOV-1997) Section of Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

REFERENCE 21 (bases 133963 to 138972; 176911 to 186244)

AUTHORS Styke, J.L., Mantie, N.J., Kalogeraki, V.S., and Winans, S.C.

TITLE Direct Submission

JOURNAL Submitted (23-DEC-1997) Microbiology, Cornell University, Ithaca, NY 14853, USA

REFERENCE 22 (bases 22855 to 39243)

AUTHORS Winans, S.C.

TITLE Direct Submission

JOURNAL Submitted (03-AUG-1998) Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

REFERENCE 23 (bases 62801 to 66985)

AUTHORS Oger, P.M.

TITLE Direct Submission

JOURNAL Submitted (29-DEC-1998) Crop Sciences, University of Illinois at Urbana-Champaign, 361 ERML, 1201, W. Gregory Dr., Urbana, IL 61801, USA

REFERENCE 24 (bases 110822 to 133968)

AUTHORS Zhu, J., and Winans, S.C.

TITLE Direct Submission

JOURNAL Submitted (18-AUG-1999) Section of Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

REFERENCE 25 (bases 1 to 194140)

AUTHORS Zhu, J., Oger, P.M., Schramm, B., Hooykaas, P.J., Farrand, S.K., and Winans, S.C.

TITLE Direct Submission

JOURNAL Submitted (07-MAR-2000) Microbiology, Cornell University, Wing Hall, Ithaca, NY 14853, USA

COMMENT On or before Jun 20, 2000 this sequence version replaced
 g1:3377769, g1:1215729, g1:1381799, g1:797350, g1:2665704,
 g1:3749889, g1:5738260, g1:2773254, g1:2773255, g1:2773256,
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source

Query Match 23.0%; Score 733.4; DB 1; Length 194140;
 Best Local Similarity 96.0%; Pred. No. 1.6e-106;
 Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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DEFINITION Sequence 2 from patent US 5689042.
ACCESSION 175097
VERSION 175097.1 GI:3011238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 709)
AUTHORS Amasino, R.M., and Gan, S.
TITLE Transgenic plants with altered senescence characteristics
JOURNAL Patent: US 5689042-A 2 18-NOV-1997;
FEATURES
Location/Qualifiers
1..709
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ORIGIN
Query Match 22.3%; Score 709; DB 6; Length 709;
Best Local Similarity 100.0%; Pred. No. 2.4e-102; Indels 0; Gaps 0;
Matches 709; Conservative 0; Mismatches 0

QY 1472 AAGCTTTAACTGACAGATGGTTCCTGTAATAAAGCAATCTTTGAATCAAACT 1531
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QY 1532 ATTGATTAGTGAAGAAAGCAAGAAAGATTCCTGTTTTATGATTAAGTATTTGAT 1591
DB 61 ATTGATTAGTGAAGAAAGCAAGAAAGATTCCTGTTTTATGATTAAGTATTTGAT 120

QY 1592 GCATGAAGGTAAGTACTGATCTACAGAAATAAAGTATTAAGTATTAAGTATTAAGT 1651
DB 121 GCATGAAGGTAAGTACTGATCTACAGAAATAAAGTATTAAGTATTAAGTATTAAGT 180

QY 1652 TGTAAAGATATTTTTCCTCAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1711
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QY 1712 TCAATTAATAAAGTCTTCTTAATAATTAATTAATTAATTAATTAATTAATTAATTA 1771
DB 241 TCAATTAATAAAGTCTTCTTAATAATTAATTAATTAATTAATTAATTAATTAATTA 300

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QY 1952 CAGGTTGATGAGATCAATAAATGGCTAGATCAAAATCAAGATCAATTAATTAATTA 2011
DB 481 CAGGTTGATGAGATCAATAAATGGCTAGATCAAAATCAAGATCAATTAATTAATTAAT 540

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DB 541 TGAATGAATGATGATCAATTAATTAATAAATGCTTTGATTTGATCAATCACTTCA 600

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DEFINITION Sequence 2 from patent US 6359197.
ACCESSION AR201517
VERSION AR201517.1 GI:20252405
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 709)
AUTHORS Amasino, R.M., Gan, S., and Noh, Y.-S.
TITLE Transgenic plants with altered senescence characteristics
JOURNAL Patent: US 6359197-A 2 19-MAR-2002;
FEATURES
Location/Qualifiers
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/organism="unknown"
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ORIGIN
Query Match 22.3%; Score 709; DB 6; Length 709;
Best Local Similarity 100.0%; Pred. No. 2.4e-102; Indels 0; Gaps 0;
Matches 709; Conservative 0; Mismatches 0

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DB 1 AAGCTTTAACTGACAGATGGTTCCTGTAATAAAGCAATCTTTGAATCAAACT 60

QY 1532 ATTGATTAGTGAAGAAAGCAAGAAAGATTCCTGTTTTATGATTAAGTATTTGAT 1591
DB 61 ATTGATTAGTGAAGAAAGCAAGAAAGATTCCTGTTTTATGATTAAGTATTTGAT 120

QY 1592 GCATGAAGGTAAGTACTGATCTACAGAAATAAAGTATTAAGTATTAAGTATTAAGT 1651
DB 121 GCATGAAGGTAAGTACTGATCTACAGAAATAAAGTATTAAGTATTAAGTATTAAGT 180

QY 1652 TGTAAAGATATTTTTCCTCAATATTAATTAATTAATTAATTAATTAATTAATTAAT 1711
DB 181 TGTAAAGATATTTTTCCTCAATATTAATTAATTAATTAATTAATTAATTAATTAAT 240

QY 1712 TCAATTAATAAAGTCTTCTTAATAATTAATTAATTAATTAATTAATTAATTAATTA 1771
DB 241 TCAATTAATAAAGTCTTCTTAATAATTAATTAATTAATTAATTAATTAATTAATTA 300

QY 1772 TGCATAAATCATCTCAAGACATATCCAACTTGCATAATCAATTAATTAATTAATTA 1831
DB 301 TGCATAAATCATCTCAAGACATATCCAACTTGCATAATCAATTAATTAATTAATTAAT 360

QY 1832 AATAAATTTTACTAGATCAAACTTCTTAATCAATCAATTAATTAATTAATTAATTAAT 1891
DB 361 AATAAATTTTACTAGATCAAACTTCTTAATCAATCAATTAATTAATTAATTAATTAAT 420

QY 1892 TAAACCCACCACTAAATTAATTAATAAATCCGAGCAAGTGAAGTAAAGACGTTGAT 1951
DB 421 TAAACCCACCACTAAATTAATTAATAAATCCGAGCAAGTGAAGTAAAGACGTTGAT 480

QY 1952 CAGGTTGATGAGATCAATAAATGGCTAGATCAAAATCAAGATCAATTAATTAATTA 2011
DB 481 CAGGTTGATGAGATCAATAAATGGCTAGATCAAAATCAAGATCAATTAATTAATTAAT 540

QY 2012 TGAATGAATGATGATCAATTAATTAATAAATGCTTTGATTTGATCAATCACTTCA 2071
DB 541 TGAATGAATGATGATCAATTAATTAATAAATGCTTTGATTTGATCAATCACTTCA 600

QY 2072 TGTGAACATTTAGCAATTAATCAATCAATTAATTTTCACTAATAAAGCCATCTCAAT 2131
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QY 2132 TCTGAAGTAAATCAATTAAGCAAGATCAATTAATTTCTCTTAATAAC 2180

Db 661 TCTGAGTATCAATTAAGAGCAAGTCATTTAATTCTTAACC 709

RESULT 15
ATTWRPTI 1983 bp DNA linear BCT 14-AUG-1995
LOCUS Agrobacterium tumefaciens pTiT37 T-DNA tmr locus.
DEFINITION
ACCESSION X00639.1 GI:944822
VERSION X00639.1
KEYWORDS cytoKlinh; plasmid.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizodiales; Rhizobium/Agrobacterium group; Agrobacterium.

REFERENCE
AUTHORS Goldberg, S.B., Flick, J.S. and Rogers, S.G.
TITLE Nucleotide sequence of the tmr locus of Agrobacterium tumefaciens
pTi T37 T-DNA
JOURNAL Nucleic Acids Res. 12 (11), 4665-4677 (1984)
MEDLINE 84247329
PUBMED 6330678
COMMENT On Aug 15, 1995 this sequence version replaced gi:39174.
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OKFPRVNAAYDFEGHPEFGMY"
1418..1422

ORIGIN
polyA_signal

Query Match 20.0%; Score 636.6; DB 1; Length 1983;
Best Local Similarity 90.8%; Pred. No. 5,7e-91;
Matches 678; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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QY 2235 GATAGCTCTGGCCAGAGAGAGGCTTCAGTCTTTCGCTTGAATCGGATCGTG 2294
DB 712 GGTAAGCTCTGGCCAGAGAGAGGCTTCAGTCTTTCGCTTGAATCGGATCGTG 771
QY 2295 TCCCAACTATACACCGAAGCGAGAGCAACAGTGGAAGAACTGAAAGAGAGAGCG 2354
DB 772 TCTGAGCTGTCAACCGAAGCGAGAGCAACAGTGGAAGAACTGAAAGAGAGCG 831
QY 2355 TCTCTACCTTGAATCGGCTCTGGTGAAGGATATCATGCAAGCAAGCAAGCTCATCA 2414
DB 832 TCTATACCTTGAATCGGCTCTGGTGAAGGATATCATGCAAGCAAGCAAGCTCATCA 891
QY 2415 TAGGCTGATGAGAGAGTATATCATGAGGCAACGAGCGGCTTATTTTGAAGGAGG 2474
DB 892 AAGCGTGATGAGGAGAGTATATCATGAGGCAACGAGCGGCTTATTTTGAAGGAGG 951
QY 2475 ATCCACCTGTGCTCAATCGATGAGGCGGAAACAGCTATTTGAGTGCAAGATTTTGTG 2534
DB 952 ATCTATCTGTGCTCAATCGATGAGGCGGAAACAGCTATTTGAGTGCAAGATTTTGTG 1011

QY 2535 GCATATTAATTCGACCAAGTTAACCCGACCAAGACCTTCATGAAGCGGCCAAGGCCG 2594
DB 1012 GCATATTAATTCGACCAAGTTAACCCGACCAAGACCTTCATGAAGCGGCCAAGGCCG 1071
QY 2595 AGTTAAGCAGATGTTGCAACCCCGCTGCAAGGCCATTTATTAAGAGTGGTTATCT 2654
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QY 2655 TTGGAATGAACCTCGGCTGAGGCCCATCTGTGAAGAGATCGATGATATGATGCCAT 2714
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QY 2895 AATGATTAAGTTAGCCCAAGCCCTGAG 2921
DB 1372 AATGATTAAGTTAGCCCAAGCCCTGAG 1398

Search completed: June 10, 2004, 05:04:27
Job time: 19497 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2004, 18:06:23 / Search time 1744 Seconds
(without alignments)
7753.449 Million cell updates/sec

Title: US-10-072-077A-1
Perfect score: 3183
Sequence: 1 gatctctctttatctca.....tatgttaccagatcgatcc 3183

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_29Jan04:*
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2: geneseq1990s:*
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4: geneseq2001as:*
5: geneseq2001bs:*
6: geneseq2002s:*
7: geneseq2003as:*
8: geneseq2003bs:*
9: geneseq2003cs:*
10: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	3183	100.0	3183	2 AAT42919
2	3178.2	99.8	3183	6 AAD33601
3	3171	99.6	3182	6 AAD33336
4	734.8	23.1	745	6 AAV69757
5	733.4	23.0	1988	6 ABR12492
6	733.4	23.0	24596	1 AAN50182
7	730.2	22.9	24593	1 AAN50226
8	714.8	22.5	723	3 AAD00619
9	712.2	22.4	747	3 AAD00624
10	709	22.3	709	6 AAT42917
11	709	22.3	709	6 AAD33337
12	701.2	22.0	723	1 AAN70790
13	569.4	17.9	723	6 AAD44425
14	536.4	16.9	3017	3 AAC86511
15	536	16.8	721	3 AAC86514
16	536	16.8	723	3 AAC86515
17	536	16.8	2722	3 AAC86508
18	536	16.8	2722	3 AAC86507
19	536	16.8	2542	3 AAC86506
20	433.4	13.6	2544	3 AAD00626
21	344.4	10.8	584	2 AATQ8641
22	262.8	8.3	7599	4 AAF25320
23	261.8	8.2	4280	4 AAF25317

24	261.8	8.2	4309	4 AAF25319
25	257.2	8.1	1829	2 AATQ29293
26	257.2	8.1	1863	2 AATQ21191
27	257.2	8.1	1863	2 AATQ4261
28	257.2	8.1	4284	2 AATQ4259
29	256.2	8.0	12982	4 AAF86432
30	256.2	8.0	15397	2 AAT58635
31	256.2	8.0	15397	2 AAT58635
32	256	8.0	5534	2 AAT43137
33	255.8	8.0	5465	2 AAT20088
34	255.6	8.0	17458	6 ABQ82142
35	255.6	8.0	17476	6 ABQ82141
36	255.6	8.0	17681	6 ABQ82143
37	255.6	8.0	18691	6 ABQ82130
38	255.2	8.0	8074	6 ABA05262
39	255	8.0	5228	4 AAF86439
40	255	8.0	6548	2 AAT39336
41	255	8.0	6548	2 AAT61394
42	255	8.0	6548	2 AAT61096
43	254.2	8.0	7492	3 AAT86441
44	254.2	8.0	2709	2 AAV44284
45	254.2	8.0	5281	6 ABL56341

ALIGNMENTS

RESULT 1
ID AAT42919 standard; DNA; 3183 BP.

AC AAT42919;
DT 18-JAN-1997 (first entry)

XX SAG12-1 promoter, isopentenyltransferase gene and NOS terminator.

XX SAG12-1; promoter; senescence-associated gene; isopentenyltransferase;

KW NOS terminator; Arabidopsis thaliana; development; gene regulation;

KW 5'-untranslated region; cytokinin biosynthesis; transgenic plant;

KW flowering; seed; fruit; crop improvement; ds.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

PH 1..2073

FT promoter

FT 1473..2073

FT promoter

FT 2074..2180

FT 5'UTR

FT CDS

FT 2181..2920

FT CDS

FT 2921..3180

FT terminator

FT 2921..3180

FT terminator

FT 2921..3180

FT terminator

FT 2921..3180

FT terminator

FT 2921..3180

FT terminator

FT 2921..3180

FT terminator

FT 2921..3180

FT terminator

FT 2921..3180

FT terminator

FT 2921..3180

FT terminator

FT 2921..3180

FT terminator

FT 2921..3180

FT terminator

FT 2921..3180

PT Senescence associated gene promoters, SAG12 and SAG13, - useful for
PT producing genetic constructs for producing transgenic plants having
PT delayed senescence.

XX Example; Page 26-27; 38bp; English.

CC The sequence represents a full-length version of the SAG12-1 promoter
CC (truncated version given in AAT42917) from an Arabidopsis thaliana
CC senescence-associated gene. The sequence also contains the SAG12-1 gene
CC 5'-untranslated region, and has been linked to a cytokinin biosynthesis
CC isopentenyltransferase gene and NOS terminator for senescence-specific
CC gene expression in a transgenic plant. The resulting transgenic plant
CC shows delayed senescence, and shows longer vegetative growth, producing
CC more flowers, seeds or fruit

XX Sequence 3183 BP; 1042 A; 527 C; 560 G; 1054 T; 0 U; 0 Other;

Query Match 100.0%; Score 3183; DB 2; Length 3183;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 GAATGATGATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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QY 901 TTTACACCGCATTTTCCCTGTAACAAGATTCATATATTTATTTATATATATATATATATAT 960
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Db 1801 TCGAAATCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
QY 1861 ATCATCAATTAATTAATGTTTACAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
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D	2041	AAAAATGCTTGAATTGATCAATCACTCATGTGAACATTAAGCAATTATCAACCTTA	2100
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Q	2221	AAGACGACGACCGGATAGCTTTGCCAGACACAGGCTTCCATCTTTGCTTGAT	2280
D	2221	AAGACGACGACCGGATAGCTTTGCCAGACACAGGCTTCCATCTTTGCTTGAT	2280
Q	2281	CGGATCAATGCTGCTCCAACTATCAACGGAAAGCGACACACAGTGAAGAAGT	2340
D	2281	CGGATCAATGCTGCTCCAACTATCAACGGAAAGCGACACACAGTGAAGAAGT	2340
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Q	2761	CTTGACGAAATATGAGAGTAAAGTATATGAGATCGCTACAGAGTATTTATCAT	2820
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D	2881	GGTCAATCGTGGATGATATAGGTATGCGCAAGCCCTGAGCTCATGCTTCAACATT	2940
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Accession	Gene	Location/Qualifiers	Length
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Qy	3061 GATGGGTTTATGATTAGAGTCCCGCAATTATACATTTAATACGGATGAAAAACAAA		3120
Db	3061 GATGGGTTTATGATTAGAGTCCCGCAATTATACATTTAATACGGATGAAAAACAAA		3120
Qy	3121 TATGCGCGCAAACTGGGATTAATTAATTCGCGCGGTGTCATCTATGTACTAGATCGAA		3180
Db	3121 TATGCGCGCAAACTGGGATTAATTAATTCGCGCGGTGTCATCTATGTACTAGATCGAA		3180
Qy	3181 TTC 3183		
Db	3181 TTC 3183		
RESULT 2			
AAD33601			
ID	AAD33601	standard; DNA; 3183 BP.	
XX	AAD33601;		
AC			
DX	01-JUL-2002 (first entry)		
DT			
XX			
DE	A. thaliana SAG12 promoter/1PT/NOS-ter construct.		
XX			
KM	Senescence associated gene; SAG-12; transgenic plant; transgenic;		
KM	senescence-specific promoter; senescence characteristic; chimeric; 1PT;		
KW	isopentenyl transferase; NOS-ter; ds.		
XX			
XX	Arabidopsis thaliana.		
OS	unidentified.		
OS	chimeric.		
XX			
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FT	5'UTR	2076..2179	
FT		/*tag= c	
FT	misc_feature	2180..2919	
FT		/*tag= d	
FT		/note= "NcoI-1PT sequence"	
FT	misc_feature	2920..3183	
FT		/*tag= e	
FT		/note= "SctI-NOS ter sequence"	
XX			
XX	US6359197-B1.		
XX			
PD	19-MAR-2002.		
XX			
PF	17-NOV-1997;	97US-00971395.	
XX			
PR	29-MAR-1995;	95US-00413135.	
XX			
PA	(WISC) WISCONSIN ALUMNI RES FOUND.		
XX			
PI	Amasino RM, Gan S, Noh Y;		
XX			
DR	WPI; 2002-291012/33.		
XX			
PT	Novel senescence associated promoter sequence connected to a protein-		
PT	coding DNA sequence useful for the creation of transgenic plants with		
XX	altered senescence characteristics.		
PS	Claim 1; Fig 3; 21pp; English.		
XX			

CC The invention relates to a genetic construct comprising senescence
CC specific promoter, preferably a senescence associated gene (SAG)-12
CC promoter operably connected to a protein-coding DNA sequence not natively
CC connected to the promoter. The senescence associated promoters are useful
CC for the creation of transgenic plants with altered senescence
CC characteristics. Genetic constructs can be inserted into plants which
CC become effective only upon plant cells entering senescence. For example,
CC a gene encoding a biosynthetic enzyme under the control of a senescence-
CC specific promoter can be inserted into a plant, without having the
CC tissues of the plant exposed to the excess of cytokinin during pre-
CC senescence growth. Then at the onset of senescence, the senescence-
CC specific promoter activates cytokinin production to alter the progression
CC of senescence in the plant. The present sequence is a chimeric construct
CC comprising Arabidopsis thaliana SAG12 promoter, isopentenyl transferase
CC (IPT) gene and NOS-ter sequence. Note: This sequence is stated to be same
CC as that shown as SEQ ID NO:1 (A033336) in Column 15-20 of the
CC specification. However the sequences differ at several positions
XX
SQ Sequence 3183 BP; 1042 A; 528 C; 559 G; 1054 T; 0 U; 0 Other;
Query Match 99.8%; Score 3178.2; DB 6; Length 3183;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3180; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GATATCTCTTTTATATTCACAAATAGCTGATGATCTTTAGAGAGGAGCACTATT 60
DB 1 GATATCTCTTTTATATTCACAAATAGCTGATGATCTTTAGAGAGGAGCACTATT 60
QY 61 CTGTGGAGACCGAGCTCTTTTATATTCAGAAACCGATTGTTATTTAGACTGAGAC 120
DB 61 CTGTGGAGACCGAGCTCTTTTATATTCAGAAACCGATTGTTATTTAGACTGAGAC 120
QY 121 AAAAAAGTAAATCGTGTATGTTTAAATTTAAATTTAGTTTCACTACGTTTGCATPAAA 180
DB 121 AAAAAAGTAAATCGTGTATGTTTAAATTTAAATTTAGTTTCACTACGTTTGCATPAAA 180
QY 181 AATGATGATGTTATCATAGCTATATAGCATGATCTTAATTTGTTTGAACCTTT 240
DB 181 AATGATGATGTTATCATAGCTATATAGCATGATCTTAATTTGTTTGAACCTTT 240
QY 241 TTTTCTCTCTTGGTGTCTTTCTTATCATAGAGAACCCATTAACATGTCAGTTCAAT 300
DB 241 TTTTCTCTCTTGGTGTCTTTCTTATCATAGAGAACCCATTAACATGTCAGTTCAAT 300
QY 301 AATTAATAAACAATTTTCCAGTTTATATAGCAACTGTTTATTAAGAAAACGTT 360
DB 301 AATTAATAAACAATTTTCCAGTTTATATAGCAACTGTTTATTAAGAAAACGTT 360
QY 361 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 ATGAACAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 ATGAACAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 AAAAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 AAAAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 GATATCTCTTCAAGAAATTTTGGCCATATGATGATGATGATGATGATGATGATGAT 600
DB 541 GATATCTCTTCAAGAAATTTTGGCCATATGATGATGATGATGATGATGATGATGAT 600
QY 601 GAGACGAGAGAAAGATTTGGGTCAATTAACAAAGAGACACTGATATAGTTGTA 660
DB 601 GAGACGAGAGAAAGATTTGGGTCAATTAACAAAGAGACACTGATATAGTTGTA 660
QY 661 CTGTGGAGACCGAGCTCTTTTATATTCAGAAACCGATTGTTATTTAGACTGAGAC 720
DB 661 CTGTGGAGACCGAGCTCTTTTATATTCAGAAACCGATTGTTATTTAGACTGAGAC 720
QY 721 TCGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780

DB 721 TCGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 761 TGTGTTCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 761 TGTGTTCATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 TACCAAGGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 TACCAAGGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 TTTACACCGCATTTTCCCTGACAAAGATTCATATATTTATTTATTAATCTCCAGTT 960
DB 901 TTTACACCGCATTTTCCCTGACAAAGATTCATATATTTATTTATTAATCTCCAGTT 960
QY 961 GACAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 GACAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 TATGCTTATCTCTCTTGTGTAAGAAACCTACATATCTATATTAATAATAATTCCT 1080
DB 1021 TATGCTTATCTCTCTTGTGTAAGAAACCTACATATCTATATTAATAATAATTCCT 1080
QY 1081 AATCATTAATTTGTAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 AATCATTAATTTGTAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 TTTATCTTACGACCAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 TTTATCTTACGACCAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 CTCTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 CTCTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 TTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 TTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 GGGAAACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 GGGAAACATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 ACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 ACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 TGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
DB 1441 TGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
QY 1501 TGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1501 TGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1561 TGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
DB 1561 TGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 1621 AATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 AATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 TATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
DB 1681 TATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1741 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800
DB 1741 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800
QY 1801 TCGAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860

Db 1801 TCGAAATCTCTATAGTACAGAAAGTAGAGAAATTAATTTTACTAGATACAAACTTCTTA 1860
 QY 1861 ATCATCATTTATTAATGTTTACAAAACTAATTAACCCACGACTAAATTAATTAATAAAT 1920
 Db 1861 ATCATCATTTATTAATGTTTACAAAACTAATTAACCCACGACTAAATTAATTAATAAAT 1920
 QY 1921 CCGAGCAAAAGTAGTAGAACAAGACTGATTCAGGTTGATGTGAGCTAAAGGCTAGC 1980
 Db 1921 CCGAGCAAAAGTAGTAGAACAAGACTGATTCAGGTTGATGTGAGCTAAAGGCTAGC 1980
 QY 1981 TATCAAAACATCAACGATCATTTAGTTATGTATGATGAATGTAGTACTTCTGTAAAC 2040
 Db 1981 TATCAAAACATCAACGATCATTTAGTTATGTATGATGAATGTAGTACTTCTGTAAAC 2040
 QY 2041 AAAAATGCTTTGATTTGATGATCAATCACTTCATGTGAACATTAGCAATTACATCACTTA 2100
 Db 2041 AAAAATGCTTTGATTTGATGATCAATCACTTCATGTGAACATTAGCAATTACATCACTTA 2100
 QY 2101 TTTTCACTATPAAACCCCATCTCAGTACCCCTTGAAGTATCAAAATTAAGACAAAAGT 2160
 Db 2101 TTTTCACTATPAAACCCCATCTCAGTACCCCTTGAAGTATCAAAATTAAGACAAAAGT 2160
 QY 2161 CATTTACTCTTCTTAAACAGATGAGACCCCTGATCTAATTTTCCGTCACCTTGACACAGA 2220
 Db 2161 CATTTACTCTTCTTAAACAGATGAGACCCCTGATCTAATTTTCCGTCACCTTGACACAGA 2220
 QY 2221 AAGACGACGACCGGATGAGTCTTTCAGCAGACAGAGGCTTCAGTCTTTCGCTTGAT 2280
 Db 2221 AAGACGACGACCGGATGAGTCTTTCAGCAGACAGAGGCTTCAGTCTTTCGCTTGAT 2280
 QY 2281 CGGCTCCATCTGCTCTCAACTATCAACCGGAAGCGGACGACCAACAGTGGAAAGAACTG 2340
 Db 2281 CGGCTCCATCTGCTCTCAACTATCAACCGGAAGCGGACGACCAACAGTGGAAAGAACTG 2340
 QY 2341 AAAAGAAACGACGCTCTCTACCTTGATGATGGGCTCTGAGGAGGATCATGACAGCC 2400
 Db 2341 AAAAGAAACGACGCTCTCTACCTTGATGATGGGCTCTGAGGAGGATCATGACAGCC 2400
 QY 2401 AAGCAAGCTCATATAGGCTGATGAGAGAGTGTATATCATATGAGGCCAACGCGGCGCTT 2460
 Db 2401 AAGCAAGCTCATATAGGCTGATGAGAGAGTGTATATCATATGAGGCCAACGCGGCGCTT 2460
 QY 2461 ATTCTTGAGGAGAGATCCACTCGTTGCTCAACTGCAATGGGCGGCAACAGTATTTGAGT 2520
 Db 2461 ATTCTTGAGGAGAGATCCACTCGTTGCTCAACTGCAATGGGCGGCAACAGTATTTGAGT 2520
 QY 2521 GCAAGATTTTCTGGGCAATATATTCGCAAGTATCCCGCAAGAGACCTTCATGAAA 2580
 Db 2521 GCAAGATTTTCTGGGCAATATATTCGCAAGTATCCCGCAAGAGACCTTCATGAAA 2580
 QY 2581 GCGGCCAAGGCGCAGATTAGCAGATGTTGCAACCCCGCTGAGGCGCATTTATTAATTCAA 2640
 Db 2581 GCGGCCAAGGCGCAGATTAGCAGATGTTGCAACCCCGCTGAGGCGCATTTATTAATTCAA 2640
 QY 2641 GAGTTGGTTTATCTTTGGAATGAACTCGGCTGAGGCGCATTTGAAAGAAATGCAATGAA 2700
 Db 2641 GAGTTGGTTTATCTTTGGAATGAACTCGGCTGAGGCGCATTTGAAAGAAATGCAATGAA 2700
 QY 2701 TATGATATGCGCATGTTGTTGCTAGCCAGAAACGATCAAGGCGCATTTATTAATTCAG 2760
 Db 2701 TATGATATGCGCATGTTGTTGCTAGCCAGAAACGATCAAGGCGCATTTATTAATTCAG 2760
 QY 2761 CTGAGCAAAATATGAAAGTATGTTAATGAGGATGCTCAGAGATTTATTCATCAT 2820
 Db 2761 CTGAGCAAAATATGAAAGTATGTTAATGAGGATGCTCAGAGATTTATTCATCAT 2820
 QY 2821 GCGCGCCAAACAGAAACAGAAATTTCCCGCAAGTAAACGCGCTTTCAGAGGATTTGAA 2880
 Db 2821 GCGCGCCAAACAGAAACAGAAATTTCCCGCAAGTAAACGCGCTTTCAGAGGATTTGAA 2880
 QY 2881 GGTGATCCGTTGGAATGATTAAGTTAGGCGCAGGCGCTGAGTGCATGCTTCAAACTTT 2940
 Db 2881 GGTGATCCGTTGGAATGATTAAGTTAGGCGCAGGCGCTGAGTGCATGCTTCAAACTTT 2940

QY 2941 GGCATPAAAGTTCTTAAAGATGAATCCGTTGCGGCTTTCGATGATATCATATTAAT 3000
 Db 2941 GGCATPAAAGTTCTTAAAGATGAATCCGTTGCGGCTTTCGATGATATCATATTAAT 3000
 QY 3001 TTCTGTTGATTAACGTTAAGCATGTAATTAATTAACATGTAATGATGACGTTATTTATGA 3060
 Db 3001 TTCTGTTGATTAACGTTAAGCATGTAATTAATTAACATGTAATGATGACGTTATTTATGA 3060
 QY 3061 GATGGGTTTATTAATGATTAAGATCCGCAATTATACATTTAATACGGATAGAAACAAA 3120
 Db 3061 GATGGGTTTATTAATGATTAAGATCCGCAATTATACATTTAATACGGATAGAAACAAA 3120
 QY 3121 TATGGCGGCAAACTGGGATTAATTAATTCGGCGGCTGATCTATGTTACTAGATCGAA 3180
 Db 3121 TATGGCGGCAAACTGGGATTAATTAATTCGGCGGCTGATCTATGTTACTAGATCGAA 3180
 QY 3181 TTC 3183
 Db 3181 TTC 3183

RESULT 3
 AAD33336
 ID AAD33336 standard; DNA; 3182 BP.
 AC AAD33336;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE A. thaliana SAG12 promoter/1PT/NOS-ter construct (alternative version).

XX Sensence associated gene; SAG-12; transgenic plant; transgenic;
 KM Sensence-specific promoter; sensence characteristic; chimeric; 1PT;
 KM 10pentenyl transferase; NOS-ter; ds.
 XX
 OS Arabidopsis thaliana.
 OS Unidentified.
 OS Chimeric.

XX US6359197-B1.
 XX
 PD 19-MAR-2002.
 XX
 PF 17-NOV-1997; 97US-00971395.
 XX
 PR 29-MAR-1995; 95US-00413135.
 XX
 PA (WISC) WISCONSIN ALUMNI RES FOUND.

XX Amasino RM, Gan S, Noh Y;
 XX
 DR WPI; 2002-291012/33.
 XX

PT Novel sensence associated promoter sequence connected to a protein-
 PT coding DNA sequence useful for the creation of transgenic plants with
 PT altered sensence characteristics.
 XX

PS Claim 1; Col 15-20; 21pp; English.

CC The invention relates to a genetic construct comprising sensence
 CC specific promoter, preferably sensence associated gene (SAG)-12
 CC promoter operably connected to a protein-coding DNA sequence not natively
 CC connected to the promoter. The sensence associated promoters are useful
 CC for the creation of transgenic plants with altered sensence
 CC characteristics. Genetic constructs can be inserted into plants which
 CC become effective only upon plant cells entering sensence. For example,
 CC a gene encoding a biosynthetic enzyme under the control of a sensence-
 CC specific promoter can be inserted into a plant, without having the
 CC tissues of the plant exposed to the excess of sensence, the sensence-
 CC sensence growth. Then at the onset of sensence, the sensence-
 CC specific promoter activates cytokinin production to alter the progression
 CC of sensence in the plant. The present sequence is an alternative

Dh	1981	TATCAAAACATCAAGCATCATTTAGTATATGATATGAATGAATGTATGTCAATTACTGTAAAC	2040
Qy	2041	AAAAATGCTTTGATTTTGATCAATCACTTCATGTGAACATTAGCAATTACATCACTTA	2100
Dh	2041	AAAAATGCTTTGATTTTGATCAATCACTTCATGTGAACATTAGCAATTACATCACTTA	2100
Qy	2101	TTTTTCTATTAATAAACCCTACTCTAGTACCGTTCTGAAAGTATCAATTTAAGCAAAAGT	2160
Dh	2101	TTTTTCTATTAATAAACCCTACTCTAGTACCGTTCTGAAAGTATCAATTTAAGCAAAAGT	2160
Qy	2161	CATTTAACCTTCTAAATAACATGAGACCCCTCATCTTAATTTTCCGTCCAACTTGACAGA	2220
Dh	2161	CATTTAACCTTCTAAATAACATGAGACCCCTCATCTTAATTTTCCGTCCAACTTGACAGA	2219
Qy	2221	AAGACGACGACCCGGATAGCTCTTGGCCAGACAGAGGCTTCCAGTCTTTTGGTTGAT	2280
Dh	2220	AAGACGACGACCCGGATAGCTCTTGGCCAGACAGAGGCTTCCAGTCTTTTGGTTGAT	2279
Qy	2281	CGGGTCCAAATCGTGTCTCAACTATCAACCGGAAGCGGACCAACAGTGAAGAAACTG	2340
Dh	2280	CGGGTCCAAATCGTGTCTCAACTATCAACCGGAAGCGGACCAACAGTGAAGAAACTG	2339
Qy	2341	AAAGGAACGACGCGCTCTACCTTGATATCGGCGCTTGGTGAAGGGTATCATCGAGCC	2400
Dh	2340	AAAGGAACGACGCGCTCTACCTTGATATCGGCGCTTGGTGAAGGGTATCATCGAGCC	2399
Qy	2401	AAGCAAGCTCATCAATAGCTGATCGAGAGGTGTATATCATAGAGCCACGCGGCTT	2460
Dh	2400	AAGCAAGCTCATCAATAGCTGATCGAGAGGTGTATATCATAGAGCCACGCGGCTT	2459
Qy	2461	ATTCTTGAAGGAGATCCACTCGTTGCTCAACTGCAATGCGCGGAAACACTATTTGGAGT	2520
Dh	2460	ATTCTTGAAGGAGATCCACTCGTTGCTCAACTGCAATGCGCGGAAACACTATTTGGAGT	2519
Qy	2521	GCAATTTTGGTGGCAATTAATTGCGCAACAAGTTACCCGACCAAGAGACCTTCATGAA	2580
Dh	2520	GCAATTTTGGTGGCAATTAATTGCGCAACAAGTTACCCGACCAAGAGACCTTCATGAA	2579
Qy	2581	GCGCGCAAGCGCAGAGTTAAGCAAGTGTGCAACCCCGCTGAGGCCATTCATTAATCA	2640
Dh	2580	GCGCGCAAGCGCAGAGTTAAGCAAGTGTGCAACCCCGCTGAGGCCATTCATTAATCA	2639
Qy	2641	GAGTTGGTTATCTTTGSAATGAACCTGCGCTGAGGCCATTCGAAAGAGATGTAGTA	2700
Dh	2640	GAGTTGGTTATCTTTGSAATGAACCTGCGCTGAGGCCATTCGAAAGAGATGTAGTA	2699
Qy	2701	TATCGATATGCAATGTTGTTGCTAGACGAGAACCAAGATCAAGGCGAGATGCTATTCAG	2760
Dh	2700	TATCGATATGCAATGTTGTTGCTAGACGAGAACCAAGATCAAGGCGAGATGCTATTCAG	2759
Qy	2761	CTTACGCAAAATATGAGAGTAAAGTTGATTAATGAGATCGCTACGAGATATTCATCAT	2820
Dh	2760	CTTACGCAAAATATGAGAGTAAAGTTGATTAATGAGATCGCTACGAGATATTCATCAT	2819
Qy	2821	GCGGCGCAACAGAGAACAGAAATTCGCCCAAGTTAACGCAAGCGCTTTCGACGATTTGAA	2880
Dh	2820	GCGGCGCAACAGAGAACAGAAATTCGCCCAAGTTAACGCAAGCGCTTTCGACGATTTGAA	2879
Qy	2881	GGTCAATCCGTTGGAATGATTAATAGTTACGCAAGCCCTGAGCTGATGTTCACAACTTT	2940
Dh	2880	GGTCAATCCGTTGGAATGATTAATAGTTACGCAAGCCCTGAGCTGATGTTCACAACTTT	2939
Qy	2941	GGCAATTAAGTTTCTTAAGATGATCTGTTGCGGCTTGGCGATGATTAATCAATTAAT	3000
Dh	2940	GGCAATTAAGTTTCTTAAGATGATCTGTTGCGGCTTGGCGATGATTAATCAATTAAT	2999
Qy	3001	TTCTGTGAATTAAGTTAAGCATGATPAATTAATTAACATGATGCAATGACGTTATTATGA	3060
Dh	3000	TTCTGTGAATTAAGTTAAGCATGATPAATTAATTAACATGATGCAATGACGTTATTATGA	3058
Qy	3061	GATGGGTTTTTATGATTAAGTCCCGCAATTAATTAACATTAAGCGGATAGAAACAATA	3120
Dh	3060	GATGGGTTTTTATGATTAAGTCCCGCAATTAATTAACATTAAGCGGATAGAAACAATA	3119

OY		3121	TATGGCGCCCAACGAGGTAAATTATGCGCGCGGTGCATCTATGTTACTAGATCGAA	3180
Db		3120	TATGGCGCGCAACTGGGATAAATTATTCGCGCGGTGTCATCTATGTTACTAGATCGAA	3179
OY		3181	TTC 3183	
Db		3180	TTC 3182	
RESULT 4				
ID	AAV69757	standard; DNA;	745 BP.	
XX	AAV69757;			
AC				
XX	01-MAR-1999	(first entry)		
DT				
XX		Iso[gentenyl] transferase ipt gene.		
DE				
XX		Iso[gentenyl] transferase; ipt gene; cytokinin; transgenic plant;		
KW		seedless fruit; tomato; watermelon; cucumber; ds.		
KW				
OS		Agrobacterium tumefaciens.		
XX				
FH	Key	Location/Qualifiers		
FT	CDS	3..725		
FT		/+tag= a		
XX				
EN	WO9849888-A1.			
XX				
PD	12-NOV-1998.			
XX				
PF	06-MAY-1998;	98MO-USO09013.		
XX				
PR	06-MAY-1997;	97US-0045725P.		
XX				
PA	(UNIV) UNIV KANSAS STATE RES FOUND.			
PI	L1 Y;			
XX				
DR	WPI; 1999-034673/03.			
XX	P-P5DB; AAM81575.			
PT		A new construct to express phytohormones in developing fruit - useful		
PT		for, e.g. producing substantially seedless fruit from transgenic plants.		
XX				
PS	Example 1; Page 31-33; 4pp; English.			
XX				
CC	This is the nucleotide sequence of the Agrobacterium tumefaciens ipt gene			
CC	that codes for isopentenyl transferase (see AAM81575), an enzyme of the			
CC	cytokinin biosynthetic pathway. A claimed DNA construct comprises either			
CC	an isopentenyl transferase or a cryptophan oxygenase (see AAM81574)			
CC	encoding sequence, operably linked to an ovary or developing fruit-			
CC	specific plant-expressible promoter (see AAV69755 and AAV69759). The			
CC	construct is used to stably integrate enzymes involved in cytokinin or			
CC	auxin biosynthesis into the plant genome to achieve a transgenic plant			
CC	(preferably tomato, cucumber or watermelon) producing seedless fruit in			
CC	the absence of pollination			
SX	Sequence 745 BP; 193 A; 185 C; 192 G; 175 T; 0 U; 0 Other;			
OY	Query Match	23.1%;	Score 734.8;	DB 2; Length 745;
Db	Best Local Similarity	99.7%;	Pred. No. 2.4e-114;	
	Matches 736; Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;
OY	2187 CCTGCATCTAATTTTTCGGTCCAACCTTGACAAGGAAGAAGCAGACCGGATAGCTCTGC	2246		
Db	8 CCTGCATCTAATTTTTCGGTCCAACCTTGACAAGGAAGAAGCAGACCGGATAGCTCTTGC	67		
OY	2247 CCAGACGACAGGCGCTTCAGTCCCTTCGCTTGATCGGGTCCCATCTGTCCTCAACTATC	2306		
Db	68 CCAGACGACAGGCGCTTCAGTCCCTTCGCTTGATCGGGTCCCATCTGTCCTCAACTATC	127		

QY 2307 AACCGGAGCGGAGCAGCAACAGTGAAGAACTGAAAGAGAGCCGCTCTACCTTGA 2366
 DB 128 AACCGGAGCGGAGCAGCAACAGTGAAGAACTGAAAGAGAGCCGCTCTACCTTGA 187
 QY 2367 TGAATCGGCTCTCTGTGAGAGGTATCTATCGAGCCAGCAAGCACTCATAGAGGTATGA 2426
 DB 188 TGAATCGGCTCTCTGTGAGAGGTATCTATCGAGCCAGCAAGCACTCATAGAGGTATGA 247
 QY 2427 GAGAGGTATATCATAGAGCCAGCAAGCGGGCTTATTTCTTGAGAGAGATCCACTCGTT 2486
 DB 248 GAGAGGTATATCATAGAGCCAGCAAGCGGGCTTATTTCTTGAGAGAGATCCACTCGTT 307
 QY 2487 GCTCAACTGTCATGCGCGGAAACAGCTATTGAGATGCAATTTTCTTGCAATATATG 2546
 DB 308 GCTCAACTGTCATGCGCGGAAACAGCTATTGAGATGCAATTTTCTTGCAATATATG 367
 QY 2547 CCACAACTTACCCGAGCCAGCAAGCACTCATAGAAAGCGGCGCAAGGCAAGATTAAGAGAT 2606
 DB 368 CCACAACTTACCCGAGCCAGCAAGCACTCATAGAAAGCGGCGCAAGGCAAGATTAAGAGAT 427
 QY 2607 GTTGCAACCCGCTGTCAGAGCCATTTATTTATTTCAAGAGTGTATTTCTTGCAATGAACC 2666
 DB 428 GTTGCAACCCGCTGTCAGAGCCATTTATTTATTTCAAGAGTGTATTTCTTGCAATGAACC 487
 QY 2667 TCGGCTGAGGCGCCATTCTGAAAGAGATGATGATATCCATATGCCATGTTGTTGCTAG 2726
 DB 488 TCGGCTGAGGCGCCATTCTGAAAGAGATGATGATATCCATATGCCATGTTGTTGCTAG 547
 QY 2727 CCAGAACCAATCAACGCGCAGATATGCTATTGAGCTTGAGCAAAATATGAGAGTAACTT 2786
 DB 548 CCAGAACCAATCAACGCGCAGATATGCTATTGAGCTTGAGCAAAATATGAGAGTAACTT 607
 QY 2787 GATTAAATGAGATCGCTGTCAGAGATTTTATTCATTCATGCGCGCAACAGCAAGAAATTTCCC 2846
 DB 608 GATTAAATGAGATCGCTGTCAGAGATTTTATTCATTCATGCGCGCAACAGCAAGAAATTTCCC 667
 QY 2847 CCAGATTAAAGGAGCGGCTTTGACGAGATTTGAAAGGTCATCCGTTCCGAATGTTAGGT 2906
 DB 668 CCAGATTAAAGGAGCGGCTTTGACGAGATTTGAAAGGTCATCCGTTCCGAATGTTAGGT 727
 QY 2907 TACGCCAGCGCTGAGCTC 2924
 DB 728 TACGCCAGCGCTGAGCTC 745
 RESULT 5
 ABR12492
 ID ABR12492 standard; DNA; 1988 BP.
 AC ABR12492;
 XX 18-JUN-2002 (first entry)
 XX
 DE Agrobacterium tumefaciens isopentenyl transferase (ipt) gene.
 XX Isopentenyl transferase; ipt; myb32; promoter; transgenic; plant;
 XX senescence; cytokinin biosynthesis; shelf life; fruit; flower; leaf;
 XX tuber; horticulture; carbon fixation; biomass; forage crop;
 XX seed production; root growth; shoot growth; root formation;
 XX apical dominance; gene; ds.
 XX Arabidopsis thaliana.
 OS
 XX
 PN WO200220772-A1.
 XX
 PD 14-MAR-2002.
 XX
 PF 30-AUG-2001; 2001WO-AU001092.
 XX
 PR 06-SEP-2000; 2000AU-00009946.
 XX
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

PA (UYLT-) UNIV LA TROBE.
 XX Spargenberg G, Lin YH, Parish RW, Li SF, Heazlewood J;
 PI Pallaighy CK;
 XX WPI; 2002-304382/34.
 DR
 XX
 PT Manipulating plant senescence, useful e.g. for increasing shelf life of
 PT fruit, comprises expressing gene involved in cytokine synthesis under
 PT control of myb gene promoter.
 PS
 XX
 PS Claim 7; Fig 2; 27pp; English.

CC The invention describes a method of manipulating senescence in a plant
 CC comprising introducing a genetic construct that includes a myb gene
 CC promoter linked to a gene encoding an enzyme involved in biosynthesis of
 CC a cytokinin, where both the promoter and the gene may be used as
 CC functionally active fragments or variants. Manipulation (specifically,
 CC delay) of senescence is used to increase shelf life of fruits, flowers,
 CC leaves and tubers in horticultural produce and cut flowers, reduce
 CC perishability of horticultural crops, improve carbon fixation (and thus
 CC yield, including biomass in forage crops) and increase seed production.
 CC Use of the myb gene promoter (unlike other promoters used for
 CC overexpression of the cytokinin biosynthesis gene) does not cause
 CC retarded root and shoot growth, failure of root formation, reduced apical
 CC dominance and reduced leaf area. This sequence represents the
 CC Agrobacterium tumefaciens isopentenyl transferase (ipt) gene, the product
 CC of which is involved in cytokinin biosynthesis
 CC
 XX
 SQ Sequence 1988 BP; 593 A; 386 C; 406 G; 603 T; 0 U; 0 Other;

Query Match 23.0%; Score 733.4; DB 6; Length 1988;
 Best Local Similarity 96.0%; Pred. No. 4,3e-114;
 Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 2139 TAATCAATTAAGAGCAAAAGTCAATTAATCTCTAAACATGAGACCTGATCTAAT 2198
 DB 647 TAATATAAATAATCAGTTGTATGATCAATATATCTCAAAAACTTAATGACCTGATCTAAT 706
 QY 2199 TTTTCGTTCACTTTGACAGGAAAGAGCAGCAGCGATGCTCTTCCAGCAGAGAG 2258
 DB 707 TTTTCGTTCACTTTGACAGGAAAGAGCAGCAGCGATGCTCTTCCAGCAGAGAG 766
 QY 2259 GCTTCCAGTCTCTTGGTTGATCGGGTCAATCGTGTCTCAACTATCAACCGAGAGCG 2318
 DB 767 GCTTCCAGTCTCTTGGTTGATCGGGTCAATCGTGTCTCAACTATCAACCGAGAGCG 826
 QY 2319 ACGACCAACAGTGAAGAACTGAAGAGAGAGCGGCTCTACTTATGATGCGGCTCT 2378
 DB 827 ACGACCAACAGTGAAGAACTGAAGAGAGAGCGGCTCTACTTATGATGCGGCTCT 886
 QY 2379 GGTGAGAGGTATATGCGCAGCAAGCAAGCTCATAGAGGTATGAGAGGTATGA 2438
 DB 887 GGTGAGAGGTATATGCGCAGCAAGCAAGCTCATAGAGGTATGAGAGGTATGA 946
 QY 2439 TCATGAGGCAACGCGCGGCTTATTTCTTGAGAGAGATTCACCTGTTGCTCAACTGAT 2498
 DB 947 TCATGAGGCAACGCGCGGCTTATTTCTTGAGAGAGATTCACCTGTTGCTCAACTGAT 1006
 QY 2499 GGGCGGAAACGCTATTGAGATGAGATTTTCTTGAGAGATTTTGGCCAGCAAGTTACC 2558
 DB 1007 GGGCGGAAACGCTATTGAGATGAGATTTTCTTGAGAGATTTTGGCCAGCAAGTTACC 1066
 QY 2559 CGACCAAGAGACCTTCATGAAAGGCGCAAGGCAAGATTAAAGAGATGTTGACACCCGCG 2618
 DB 1067 CGACCAAGAGACCTTCATGAAAGGCGCAAGGCAAGATTAAAGAGATGTTGACACCCGCG 1126
 QY 2619 TGAAGGCAATTTATATTCAGAGTGTGTTATCTTTGGAATGAACCTCGGCTGAGGCG 2678
 DB 1127 TGAAGGCAATTTATATTCAGAGTGTGTTATCTTTGGAATGAACCTCGGCTGAGGCG 1186
 QY 2679 CATTTGAAGAGATGATGATATGATATGATGATGATGATGATGATGATGATGATGATGAT 2738

Db 1187 CATTTCGAAAAGATGCGATGATGATGCGATGTTGTTGCTTACCGCAAGAACCGAT 1246
QY 2739 CACGGCAGATATGCTATGTCAGCTTGAACGAAATATGGAAGTAAGTTAATGAGAT 2798
Db 1247 CACGGCAGATATGCTATGTCAGCTTGAACGAAATATGGAAGTAAGTTAATGAGAT 1306
QY 2799 CGCTCAGAGATATGCTATGTCAGCTTGAACGAAATATGGAAGTAAGTTAATGAGAT 2858
Db 1307 CGCTCAGAGATATGCTATGTCAGCTTGAACGAAATATGGAAGTAAGTTAATGAGAT 1366
QY 2859 AGCGGCTTTCAGAGATATGTCAGCTTGAACGAAATATGGAAGTAAGTTAATGAGAT 2918
Db 1367 AGCGGCTTTCAGAGATATGTCAGCTTGAACGAAATATGGAAGTAAGTTAATGAGAT 1426
QY 2919 GAG 2921
Db 1427 GCG 1429

RESULT 6
ID AANS0182 standard; DNA; 24596 BP.
AANS0182;
AC AANS0182;
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 17-OCT-1991 (first entry)

DE Complete nucleotide sequence of the T-DNA region of the octopine Ti
DE plasmid pTi15955.
XX
KM Plant vector; transformation-inducing principle (TiP) gene;
KM octopine Ti plasmid; ss.
XX
OS Agrobacterium tumefaciens; ATCC 15955.
XX
PN EP145338-A.
PD 19-JUN-1985.
PF 16-NOV-1984; 84EP-00307969.
PR 18-NOV-1983; 83US-00553786.
XX
PA (AGRK) AGRIGENETICS RES ASSOC LTD.
PA (LUBR) LUBRIZOL GENETICS INC.
XX
PI Barker RF, Kemp JD;
PI WPI, 1985-148223/25.
XX
PT New DNA vectors contg. T-DNA sequence of octopine Ti plasmid - for
PT expression in plant cells to confer desirable properties to plants and
PT their cells.
PS Claim 28; Fig 1; 87pp; English.

CC The inventors claim a vector contg. a transformation-inducing principle
CC (TiP) gene from Ti plasmid pTi15955. The sequence of the T-DNA of the
CC octopine-type Ti plasmid has fourteen open reading frames bounded by
CC eukaryotic promoters, ribosome binding sites, and polyadenylation sites.
CC With the vectors, expression of structural foreign genes in plant cells
CC is promoted. The gene esp. encodes an insecticidal toxin identical to or
CC derived from the crystal protein of *Bacillus thuringiensis*. (Updated on
CC 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise
CC OS field)
XX
SQ Sequence 24596 BP; 6534 A; 5510 C; 5793 G; 6759 T; 0 U; 0 Other;

Query Match 23.0%; Score 733.4; DB 1; Length 24596;
Best Local Similarity 96.0%; Pred. No. 4.9e-114;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 2139 TAATCAATTAAGAAGCAAAAGCTATTACTTCTTAAACCATGACCCCTGCATCTAAT 2198
Db 8728 TAATATATAAATCAAGTTTGTATTCATATATCTCGAAAACTATGAGACCTGCATCTAAT 8787
QY 2199 TTTCGGTCCCACTTTCAGAGAAAGACGACGCGGAGTAGCTCTTCCAGACAGACAG 2258
Db 8788 TTTCGGTCCCACTTTCAGAGAAAGACGACGCGGAGTAGCTCTTCCAGACAGACAG 8847
QY 2259 GCTTCAGTCCCTTTCGCTTATCGGGTCAATCGTGTCTTCACTATCAACCGGAAGCG 2318
Db 8848 GCTTCAGTCCCTTTCGCTTATCGGGTCAATCGTGTCTTCACTATCAACCGGAAGCG 8907
QY 2319 ACGAACCAACGTGGAAGAACTGAAGAGAGAGAGCGGCTCTTCACTTGAATGCGCCCT 2378
Db 8908 ACGAACCAACGTGGAAGAACTGAAGAGAGAGAGCGGCTCTTCACTTGAATGCGCCCT 8967
QY 2379 GGTGAGGATATCATGCGAGCAAGAGCTCATCATAGGCTGATCGAGAGGTGTATA 2438
Db 8968 GGTGAGGATATCATGCGAGCAAGAGCTCATCATAGGCTGATCGAGAGGTGTATA 9027
QY 2439 TCATGAGGCCAACGCGCGGCTTATTTCTGAGAGAGATCCACTGTTGCTCAACTGCAT 2498
Db 9028 TCATGAGGCCAACGCGCGGCTTATTTCTGAGAGAGATCCACTGTTGCTCAACTGCAT 9087
QY 2499 GCGCGGAAACAGCTATTGAGATGCAATTTTCTGTCATATTTTGGCCCAAGTTACC 2558
Db 9088 GCGCGGAAACAGCTATTGAGATGCAATTTTCTGTCATATTTTGGCCCAAGTTACC 9147
QY 2559 CGACCAAGAGACCTTCATGAAAGCGGCGAGGCGAGAGTTAAGAGATGTTGCAACCCCGC 2618
Db 9148 CGACCAAGAGACCTTCATGAAAGCGGCGAGGCGAGAGTTAAGAGATGTTGCAACCCCGC 9207
QY 2619 TGCAGGCCATTCTATATTTCAAGAGTTGTTTATCTTGAATGAACCTCGCTGAGGCC 2678
Db 9208 TGCAGGCCATTCTATATTTCAAGAGTTGTTTATCTTGAATGAACCTCGCTGAGGCC 9267
QY 2679 CATTCTGAAGAGATCGATGATATCGATATGCAATGTTGTTGTCAGCCCAAGCAAT 2738
Db 9268 CATTCTGAAGAGATCGATGATATCGATATGCAATGTTGTTGTCAGCCCAAGCAAT 9327
QY 2739 CACGGCAGATATGCTATGTCAGCTTGAACGAAATATGGAAGTAAGTTAATGAGAT 2798
Db 9328 CACGGCAGATATGCTATGTCAGCTTGAACGAAATATGGAAGTAAGTTAATGAGAT 9387
QY 2799 CGCTCAGAGATATGCTATGTCAGCTTGAACGAAATATGGAAGTAAGTTAATGAGAT 2858
Db 9388 CGCTCAGAGATATGCTATGTCAGCTTGAACGAAATATGGAAGTAAGTTAATGAGAT 9447
QY 2859 AGCGGCTTTCAGAGATATGTCAGCTTGAACGAAATATGGAAGTAAGTTAATGAGAT 2918
Db 9448 AGCGGCTTTCAGAGATATGTCAGCTTGAACGAAATATGGAAGTAAGTTAATGAGAT 9507
QY 2919 GAG 2921
Db 9508 GCG 9510

RESULT 7
ID AANS0226 standard; DNA; 24593 BP.
AANS0226;
AC AANS0226;
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-OCT-1991 (first entry)

DE Sequence of opine synthase gene.
DE Plant vector; Ti plasmid; T-DNA; ss.
KM Agrobacterium tumefaciens; Ti plasmid.
OS

XX EPI40556-A.
 XX 08-MAY-1985.
 XX 12-SEP-1984; 84EP-00306233.
 XX 14-SEP-1983; 83US-00532280.
 XX (AGRI) AGRIGENETICS RES ASSOC LTD.
 XX (LUBR) LUBRIZOL GENETICS INC.
 XX Dahl GA, Sutton DW, Barker RF;
 XX WPI; 1985-112088/19.
 XX
 XX Plasmid contg. opine synthase gene for selection - and foreign DNA,
 XX useful as vector for transforming plant cells.
 XX
 XX Disclosure; Page 212-217; 69pp; Japanese.
 XX
 XX plant cells (and protoplasts) and plasmids contg. the DNA fragment which
 XX includes an opine synthase gene plus a gene for antibiotic resistance are
 XX claimed. These plasmids provide max. efficiency for transfer of foreign
 XX genes and can be amplified in the plant genome. They do not contain genes
 XX specifying tumour formation and will not spread antibiotic resistance
 XX throughout the plant population. (Updated on 25-MAR-2003 to correct PF
 XX field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-
 XX 2003 to standardise OS field)
 XX
 XX Sequence 24593 BP; 6554 A; 5493 C; 5787 G; 6759 T; 0 U; 0 Other;

Query Match 22.9%; Score 730.2; DB 1; Length 24593;
 Best Local Similarity 95.8%; Pred. No. 1.7e-113;
 Matches 750; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 2139 TAAATCAATTAAGACCAAGCTATTACTTCTTAACCAATGAGACCTGCTCAATCTAT 2198
 DB 8728 TAAATCAATTAAGACCTATTGTTATCAATATCTGCAAAAACCTTAGAGACCTGCTAT 8787
 QY 2199 TTTGCTGCACTTGCACAGAGAAAGACGACGCGCTAGCTCTTGCCAGACAGAG 2258
 DB 8788 TTTGCTGCACTTGCACAGAGAAAGACGACGCGCTAGCTCTTGCCAGACAGAG 8847
 QY 2259 GCTTCAGTCTCTTGGCTTGAATCGGTCCTCAATCGTCTCAATATCAACCGAAGCG 2318
 DB 8848 GCTTCAGTCTCTTGGCTTGAATCGGTCCTCAATCGTCTCAATATCAACCGAAGCG 8907
 QY 2319 ACGACCAACAGTGAAGAACTGAAGAAAGACGCGCTCTCACTTGAATCGGCTCT 2378
 DB 8908 ACGACCAACAGTGAAGAACTGAAGAAAGACGCGCTCTCACTTGAATCGGCTCT 8967
 QY 2379 GGTGAGGGTATCATCGACGCAAGCTCATATGAGTGAAGTATATA 2438
 DB 8968 GGTGAGGGTATCATCGACGCAAGCTCATATGAGTGAAGTATATA 9027
 QY 2439 TCATGAGGCAACGCGGCTTATCTTGAAGAGATCACTCTGCTCAATGCAAT 2498
 DB 9028 TCATGAGGCAACGCGGCTTATCTTGAAGAGATCACTCTGCTCAATGCAAT 9087
 QY 2499 GGGCGCAACAGCTATGAGAGTGCAGATTTTGTGGCAATATTTCCGCAACAGTTACC 2558
 DB 9088 GGGCGCAACAGCTATGAGAGTGCAGATTTTGTGGCAATATTTCCGCAACAGTTACC 9147
 QY 2559 CGACCAAGAGACCTTATGAAAGCGGCAAGGCAAGGCTTAAGAGATTTGCAACCCGCG 2618
 DB 9148 CGACCAAGAGACCTTATGAAAGCGGCAAGGCAAGGCTTAAGAGATTTGCAACCCGCG 9207
 QY 2619 TGCAGGCAATCTATATTCAGAGTGTGTTATCTTGAATGAACCTGCGCTGAGGCC 2678
 DB 9208 TGCAGGCAATCTATATTCAGAGTGTGTTATCTTGAATGAACCTGCGCTGAGGCC 9267
 QY 2679 CATTTGAAAGAGATGATGATATGATATGCAATGTTGTTGCTAGGCAAGAACAGAT 2738

DB 9268 CATTTGAAAGAGATGATGATATGATATGCAATGTTGTTGCTAGGCAAGAACAGAT 9327
 QY 2739 CACGCAAGATATGCTATTTGACGCTTGAACCAATATGAAAGTATGATTAATGGGAT 2798
 DB 9328 CACGCAAGATATGCTATTTGACGCTTGAACCAATATGAAAGTATGATTAATGGGAT 9387
 QY 2799 CGCTCAGAGTATTTATCATCGACGCGCAACAGAGCAAGAAATCCCAAGTTAACGC 2858
 DB 9388 CGCTCAGAGTATTTATCATCGACGCGCAACAGAGCAAGAAATCCCAAGTTAACGC 9447
 QY 2859 ACCCGCTTTCAGAGATTCGAAGTGCATCGTTGGATGTATTAAGTTACGACCCCT 2918
 DB 9448 ACCCGCTTTCAGAGATTCGAAGTGCATCGTTGGATGTATTAAGTTACGACCCCT 9507
 QY 2919 GAG 2921
 DB 9508 GCG 9510

RESULT 8
 AAD00619
 ID AAD00619 standard; DNA; 723 BP.
 AC AAD00619;
 AC 29-AUG-2000 (first entry)
 DT 29-AUG-2000 (first entry)
 DE Agrobacterium tumefaciens T-DNA gene, ipt.
 XX iaam; iaah; ipt; T-DNA; transferred DNA; gall-disease resistance; BR;
 KW bacterial resistance construct; untranslatable RNA; tumour; oncogene;
 KM cytokinin; plant growth hormone; da.
 XX Agrobacterium tumefaciens.
 OS
 XX WO200026346-A1.
 EN 11-MAY-2000.
 PD 04-NOV-1999; 99WO-US026100.
 PF 05-NOV-1998; 98US-0107185P.
 PR (UWOR-) UNIV OREGON STATE.
 PA Ream W, Mok MC, Lee H;
 PI WPI; 2000-365599/31.
 PT Gall resistant plants generated by transforming cells with an
 XX untranslatable nucleic acid homologous to a gall disease-causing gene.
 DB Claim 2; Page 46; 49pp; English.
 PS
 XX The patent discloses a method for producing plants resistant to gall
 CC disease, induced by Agrobacterium infection, by transformation with a
 CC bacterial resistance (BR) construct capable of eliciting co-suppression.
 CC The construct encodes an untranslatable RNA molecule, that is highly
 CC homologous to the tumour or gall disease-causing genes iaam, iaah and ipt
 CC of Agrobacterium tumefaciens. These oncogenes are modified by
 CC introduction of premature termination codons or frameshift mutations, to
 CC inhibit their expression. This method is used to reduce susceptibility of
 CC plants to gall diseases. The present DNA sequence is the Agrobacterium
 CC tumefaciens T-DNA (transferred DNA) gene ipt, required for cytokinin
 CC production. It encodes an enzyme that converts adenosine monophosphate
 CC (AMP) into isopentenyl adenosine monophosphate, a cytokinin. The
 CC overproduction of these plant growth hormones results in gall formation
 XX
 SO Sequence 723 BP; 190 A; 175 C; 187 G; 171 T; 0 U; 0 Other;
 Query Match 22.5%; Score 714.8; DB 3; Length 723;
 Best Local Similarity 99.7%; Pred. No. 5.5e-111;


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Db      558 CAGAACGATCAGCGAGATGATGCTGACGCTTGACGCAAAATATGAGAGTAAGTTG 617
Qy      2788 ATTAATGGATCGCTCAGAGATATTCATCATGCGGCCACAGAAAGAAATTTCCC 2847
Db      618 ATTAATGGATCGCTCAGAGATATTCATCATGCGGCCACAGAAAGAAATTTCCC 677
Qy      2848 CAAATTAAGCGAGCGCTTTGACGATTCGAAAGATCATCGTTCCGATGTAATTG 2904
Db      678 CAAATTAAGCGAGCGCTTTGACGATTCGAAAGATCATCGTTCCGATGTAATTG 734

RESULT 10
AAT42917
ID      AAT42917 standard; DNA; 709 BP.
XX
AC      AAT42917;
XX
DT      18-JAN-1997 (first entry)
XX
DE      SAG12-1 promoter from senescence-associated gene.
XX
KM      SAG12-1; promoter; senescence-associated gene; development;
KM      Arabidopsis thaliana; gene regulation; 5'-untranslated region;
KM      cytokinin biosynthesis; isopentenyltransferase; transgenic plant;
KM      flowering; seed; fruit; crop improvement; ds.
XX
OS      Arabidopsis thaliana.
XX
XX      Key      Location/Qualifiers
XX      FT      promoter      1..602
XX      FT      5'UTR      /*tag= a
XX      FT      /*tag= b
XX      EN      MO9629858-A1.
XX
XX      03-OCT-1996.
XX
XX      20-FEB-1996; 96MO-US002313.
XX
XX      29-MAR-1995; 95US-00413135.
XX
XX      (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX      Amino RM, Gan S;
XX
XX      MPI, 1996-45487/45.
XX
XX      Senescence associated gene promoters, SAG12 and SAG13, - useful for
XX      producing genetic constructs for producing transgenic plants having
XX      delayed senescence.
XX
XX      Claim 2; Page 28; 38pp; English.
XX
XX      The sequence represents a truncated version of the SAG12-1 promoter
XX      (AAT42919) from an Arabidopsis thaliana senescence-associated gene. The
XX      sequence also contains part of the SAG12-1 gene 5'-untranslated region.
XX      The sequence has all regulatory signals required for senescence-specific
XX      gene expression, and may be operably linked to a cytokinin biosynthesis
XX      isopentenyltransferase gene in a vector for expression in a transgenic
XX      plant. The resulting transgenic plant shows delayed senescence, and shows
XX      longer vegetative growth, producing more flowers, seeds or fruit
XX
XX      Sequence 709 BP; 279 A; 110 C; 86 G; 234 T; 0 U; 0 Other;
XX
Query Match      22.3%; Score 709; DB 2; Length 709;
Best Local Similarity 100.0%; Pred. No. 5.2e-110; Indels 0; Gaps 0;
Matches 709; Conservative 0; Mismatches 0;
Qy      1472 AAGCTTTTACTTGACGAGATGTTCTCTTGATTAATTAACAGATCTTTGAATCAACT 1531
Db      1 AAGCTTTTACTTGACGAGATGTTCTCTTGATTAATTAACAGATCTTTGAATCAACT 60

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Qy      1532 ATTGATTTAGTGAAGAAAGCAAGAGATTCCTTGTTTATAGTATGATTTGAT 1591
Db      61 ATTTGATTTAGTGAAGAAAGCAAGAGATTCCTTGTTTATAGTATGATTTGAT 120
Qy      1592 GCATGAAGAGTACTACGACTACAGAAAAATTAACATGATGATGATGATGATGATGAT 1651
Db      121 GCATGAAGAGTACTACGACTACAGAAAAATTAACATGATGATGATGATGATGATGAT 180
Qy      1652 TGTAAAGTATTTTTCCTCAATTAATTTATCTCATGATGATGATTTTTCCTCAATTA 1711
Db      181 TGTAAAGTATTTTTCCTCAATTAATTTATCTCATGATGATGATTTTTCCTCAATTA 240
Qy      1712 TCAATTTAAAGTCTTCTTCAATTAATTTATTTAATTAATTAATTAATTAATTAATTA 1771
Db      241 TCAATTTAAAGTCTTCTTCAATTAATTTATTTAATTTAATTAATTAATTAATTAATTA 300
Qy      1772 TGCAAAACATCATCAACACATATCCAACTTCGAAATCTCTATATGATACAAAGTAGAA 1831
Db      301 TGCAAAACATCATCAACACATATCCAACTTCGAAATCTCTATATGATACAAAGTAGAA 360
Qy      1832 AATTAATTTTACTAGATACAAACTTCTCTATATGATATTAATTAATTAATTAATTAAT 1891
Db      361 AATTAATTTTACTAGATACAAACTTCTCTATATGATATTAATTAATTAATTAATTAAT 420
Qy      1892 TAAACCCACGACTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1951
Db      421 TAAACCCACGACTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480
Qy      1952 CAGTTGATGATAGACTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2011
Db      481 CAGTTGATGATAGACTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
Qy      2012 TGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2071
Db      541 TGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Qy      2072 TGTGAACATTAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2131
Db      601 TGTGAACATTAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
Qy      2132 TCTGAAGTAAATCAAAATTAAGCAAAAGTCAATTAATTTCTCTTAATTAATTAAT 2180
Db      661 TCTGAAGTAAATCAAAATTAAGCAAAAGTCAATTAATTTCTCTTAATTAATTAAT 709

RESULT 11
AAD33337
ID      AAD33337 standard; DNA; 709 BP.
XX
XX      AAD33337;
XX
XX      01-JUN-2002 (first entry)
XX
XX      Arabidopsis thaliana truncated SAG12 promoter.
XX
XX      Senescence associated gene; SAG-12; transgenic plant; transgenic;
XX      senescence-specific promoter; senescence characteristic; ds.
XX
XX      Arabidopsis thaliana.
XX
XX      Key      Location/Qualifiers
XX      FT      promoter      1..604
XX      FT      /*tag= a
XX      FT      /*tag= "SAG12 promoter fragment"
XX      FT      5'UTR      605..709
XX      FT      /*tag= b
XX
XX      US6359197-B1.
XX
XX      19-MAR-2002.
XX
XX      17-NOV-1997; 97US-00971395.
XX

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PR 29-MAR-1995; 95US-00413135.
 XX (WISC) WISCONSIN ALUMNI RES FOUND.
 XX Amasino RM, Gan S, Noh Y;
 PI WPI; 2002-291012/33.
 XX
 DR Novel senescence associated promoter sequence connected to a protein-
 PT coding DNA sequence useful for the creation of transgenic plants with
 PT altered senescence characteristics.
 XX
 PS Example; Col 17-20; 21pp; English.
 XX
 CC The invention relates to a genetic construct comprising senescence
 CC specific promoter, preferably senescence associated gene (SAG)-12
 CC promoter operably connected to a protein-coding DNA sequence not natively
 CC connected to the promoter. The senescence associated promoters are useful
 CC for the creation of transgenic plants with altered senescence
 CC characteristics. Genetic constructs can be inserted into plants which
 CC become effective only upon plant cells entering senescence. For example,
 CC a gene encoding a biosynthetic enzyme under the control of a senescence-
 CC specific promoter can be inserted into a plant, without having the
 CC tissues of the plant exposed to the excess of cytokinin during pre-
 CC senescence growth. Then at the onset of senescence, the senescence-
 CC specific promoter activates cytokinin production to alter the progression
 CC of senescence in the plant. The present sequence is Arabidopsis thaliana
 CC truncated SAG12 promoter
 XX
 XX Sequence 709 BP; 279 A; 110 C; 86 G; 234 T; 0 U; 0 Other;
 SQ
 Query Match 22.3%; Score 709; DB 6; Length 709;
 Best Local Similarity 100.0%; Pred. No. 5.2e-110;
 Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1472 AAGCTTTAACTTGACGAGATGGTCTCTTGGAATTAACGAACTTTGAATTCAACT 1531
 DB 1 AAGCTTTAACTTGACGAGATGGTCTCTTGGAATTAACGAACTTTGAATTCAACT 60
 QY 1532 ATTGATAGTGAAGAAAGCAAGAAAGATCTCTGTTTATGATAGTATTTGAT 1591
 DB 61 ATTGATAGTGAAGAAAGCAAGAAAGATCTCTGTTTATGATAGTATTTGAT 120
 QY 1592 GCATGAAGAGTACTGCTACTACAGAAATAAACAATGATAGTACTGATCAGCA 1651
 DB 121 GCATGAAGAGTACTGCTACTACAGAAATAAACAATGATAGTACTGATCAGCA 130
 QY 1652 TGTAAAGATTTTTTCCAAATAATTTACTCATGATGATTTTTTTTTTGAATG 1711
 DB 181 TGTAAAGATTTTTTCCAAATAATTTACTCATGATGATTTTTTTTTTGAATG 240
 QY 1712 TCAATTAATAAGCTTCTTAATTAATTTAATTAATTAATTAATTAATTAATTTA 1771
 DB 241 TCAATTAATAAGCTTCTTAATTAATTTAATTAATTAATTAATTAATTAATTTA 300
 QY 1772 TSCAAAACATCATCAACATATCCAACTTCGAAATCTCTATAGTACCAAGTAGAGA 1831
 DB 301 TSCAAAACATCATCAACATATCCAACTTCGAAATCTCTATAGTACCAAGTAGAGA 360
 QY 1832 AATAAATTTTACTAGTACAAACTTCTATATCATCAATTAATTAATTTACAAACTAAT 1891
 DB 361 AATAAATTTTACTAGTACAAACTTCTATATCATCAATTAATTAATTTACAAACTAAT 420
 QY 1892 TAAACCCACACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1951
 DB 421 TAAACCCACACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
 QY 1952 CAGGTGATGATGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2011
 DB 481 CAGGTGATGATGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
 QY 2012 TGAATGAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2071

DB 541 TGAATGAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
 QY 2072 TGTGAACATTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2131
 DB 601 TGTGAACATTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
 QY 2132 TGTGAACATTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2180
 DB 661 TGTGAACATTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 709
 RESULT 12
 AAN70790
 ID AAN70790 standard; DNA; 723 BP.
 XX
 AC AAN70790;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-OCT-2002 (revised)
 DT 19-MAR-1991 (first entry)
 XX
 DE Sequence of tmr gene found in the Eco RI fragment of the Agrobacterium
 DE tumefaciens Ti plasmid.
 XX
 KM Cytokinin biosynthetic enzyme; trans-zeatin; phytohormone; ss.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..723
 FT /*tag= a
 FT
 XX AUN770154-A.
 XX 24-SEP-1987.
 XX 18-MAR-1987; 87AU-00070154.
 XX 19-MAR-1986; 86US-00841464.
 XX 11-APR-1986; 86US-00850963.
 XX (UNOR-) UNIV OREGON STATE.
 XX
 PI Morris RO, Regier DA;
 XX WPI; 1987-313994/45.
 DR P-PSDB; AAP70484.
 XX
 PT New recombinant DNA molecules - for prodn. of cytokinin(s) in good yields
 PT by cultivating Escherichia coli transformants.
 XX
 PS Example; Fig 5; 59pp; English.
 XX
 CC tmr is a designation for a gene which codes for a cytokinin biosynthetic
 CC enzyme and which can be found in the EcoRI fragment of the Agrobacterium
 CC tumefaciens Ti plasmid. tzs is a designation for a gene which codes for a
 CC cytokinin biosynthetic enzyme and which can be found in or near the vir
 CC region of the Agrobacterium tumefaciens Ti plasmid pTiC58. ptz is a
 CC designation for a gene which codes for a cytokinin biosynthetic enzyme
 CC and which can be found in the larger (105 kb) plasmid of P. savastanoi
 CC strain 1006. When tmr and tzs are included in the same plasmid, there is
 CC a good increase in trans-zeatin yield. (Updated on 03-OCT-2002 to add
 CC missing OS field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 723 BP; 191 A; 175 C; 186 G; 171 T; 0 U; 0 Other;
 Query Match 22.0%; Score 701.2; DB 1; Length 723;
 Best Local Similarity 99.4%; Pred. No. 1.1e-108;
 Matches 714; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 2188 CTGACATTAATTTGCTCAACTTGACAGG-AAAGACGACGACCGGATGCTTTC 2246

```

Db      6 CTGCATTAATTTTCGCTCCACTTGCACAGAAAAACAGACGCCGATAGCTTTGC 65
QY      2247 CCAGCAGACAGAGGCTTCAGTCTTTGCTTGATCGGGTCCATCGTGTCTCTCAATATC 2306
Db      66 CCAGCAGACAGAGGCTTCAGTCTTTGCTTGATCGGGTCCATCGTGTCTCTCAATATC 125
QY      2307 AACCGGAAGCGGACGACCAACATGTGGAAGAACTGAAAAGAAACAGCGGTCTCTCACTTGA 2366
Db      126 AACCGGAAGCGGACGACCAACATGTGGAAGAACTGAAAAGAAACAGCGGTCTCTCACTTGA 185
QY      2367 TGATCGGCTCTGGTGGAGGGGATCATGCGACCAAGCACTCATCATGAGCTGATCGA 2426
Db      186 TGATCGGCTCTGGTGGAGGGGATCATGCGACCAAGCACTCATCATGAGCTGATCGA 245
QY      2427 GGAGGTATTAATCATATGAGGCCAACAGCGGGCTTATTTCTTGAGGAGGATCCACTGCTT 2486
Db      246 GGAGGTATTAATCATATGAGGCCAACAGCGGGCTTATTTCTTGAGGAGGATCCACTGCTT 305
QY      2487 GCTCACTGCACTGGCGGCGAAGAGCTATTTGAGTGCAGATTTTCTTGCCATTTATTTGC 2546
Db      306 GCTCACTGCACTGGCGGCGAAGAGCTATTTGAGTGCAGATTTTCTTGCCATTTATTTGC 365
QY      2547 CCACAAGTTACCCGACCAAGAGACCTTCATGAAAGCGGCAAGGCCAGAGTTAAGCAGAT 2606
Db      366 CCACAAGTTACCCGACCAAGAGACCTTCATGAAAGCGGCAAGGCCAGAGTTAAGCAGAT 425
QY      2607 GTTGCACCCCGCTGCAGGCCATTCATTAATTCAGAGTTGGTTATCTTTGGAATGAAC 2666
Db      426 GTTGCACCCCGCTGCAGGCCATTCATTAATTCAGAGTTGGTTATCTTTGGAATGAAC 485
QY      2667 TGGGCTGAGGCCATTTTCGAAAAGATGATGATGATGATGATGATGATGATGATGATGATG 2726
Db      486 TGGGCTGAGGCCATTTTCGAAAAGATGATGATGATGATGATGATGATGATGATGATGATG 545
QY      2727 CCAGAACCAGATCAGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2786
Db      546 CCAGAACCAGATCAGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 605
QY      2787 GATTAATGGGATCGCTCAGAGATTTTCATCCATGCGGCGCAACAGAAATATTCCTCC 2846
Db      606 GATTAATGGGATCGCTCAGAGATTTTCATCCATGCGGCGCAACAGAAATATTCCTCC 665
QY      2847 CCAAGTTAACGACGCCGCTTTGACGAGATTCGAAAGTCAATCCGTCGGAAATGATAG 2904
Db      666 CCAAGTTAACGACGCCGCTTTGACGAGATTCGAAAGTCAATCCGTCGGAAATGATAG 723

RESULT 13
AAD44425
ID      AAD44425 standard; DNA; 613 BP.
XX
AC      AAD44425;
XX
DT      13-DEC-2002 (first entry)
XX
DB      pGL471 construct comprising SAG12-35S promoter DNA.
XX
XX      Cauliflower mosaic virus 35S RNA; 35S; promoter; transgenic plant; OPR;
XX      peanut chlorotic streak caulimovirus full length transcript promoter;
XX      PCISV; 12-oxophytodienoic acid-100, 11-reductase gene promoter; SAG12;
XX      transgenic; CaMV; chimeric; ds.
XX
OS      Cauliflower mosaic virus.
OS      Unidentified.
OS      Chimeric.
XX
PN      US6388170-B1.
XX
XX      14-MAY-2002.
PD
XX      07-APR-2000; 2000US-00545244.
PF
XX      07-APR-2000; 2000US-00545244.
PR

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XX (KENT) UNIV KENTUCKY RES FOUND.

XX Gan S, Xie M, He Y,

XX WPI, 2002-442888/47.

PT Bi-directional promoter with common promoter linked in opposite
PT orientation to minimal promoter, useful to direct expression of
PT polynucleotide which confers agronomically significant trait to
PT transgenic plant.

PS Disclosure; Col 15-16; 16pp; English.

CC The invention relates to an artificial nucleic acid construct comprising
CC a bi-directional promoter having a minimal promoter operably linked in
CC opposite orientation 5' to a common promoter, where each promoter is
CC either cauliflower mosaic virus (CaMV) 35S RNA promoter (35S), peanut
CC chlorotic streak caulimovirus full length transcript promoter (PCISV),
CC Arabidopsis 12-oxophytodienoic acid-100, 11-reductase gene promoter (OPR)
CC or SAG12, and where each end of the bi-directional promoter is operably
CC linked to a polynucleotide encoding a polypeptide. The construct is used
CC to produce a transgenic plant which has an agronomically-significant
CC trait. The present sequence is pGL471 construct comprising SAG12-35S
CC promoter DNA

SQ Sequence 613 BP; 241 A; 100 C; 64 G; 208 T; 0 U; 0 Other;

Query Match. 17.9%; Score 569.4; DB 6; Length 613;

Best Local Similarity 99.8%; Pred. No. 1.4e-86;

Matches 570; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      1604 CCTACGTCTACAGAAATAATTAACATGATAGTATGATGATGATGATGATGATGATGATG 1663
Db      5 CTGAGTACTCAAGAAATAATTAACATGATAGTATGATGATGATGATGATGATGATGATG 64
QY      1664 TTTTCCAAATTAATTTATCTCATGATGATTTTTTTTTTTTGAATGTCATTAATAAT 1723
Db      65 TTTTCCAAATTAATTTATCTCATGATGATTTTTTTTTTTTGAATGTCATTAATAAT 124
QY      1724 GCTTTCTTAATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1783
Db      125 GCTTTCTTAATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 184
QY      1784 TCAACACATTCACACTCGAAATCTCATAGTACACAGATGAGAAATTAATTTTAC 1843
Db      185 TCAACACATTCACACTCGAAATCTCATAGTACACAGATGAGAAATTAATTTTAC 244
QY      1844 TAGATACAACTCTCTAATCATCAATTAATTAATTTTCAAAATCAATTAATTAATTAATTA 1903
Db      245 TGATACAACTCTCTAATCATCAATTAATTAATTTTCAAAATCAATTAATTAATTAATTAAT 304
QY      1904 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1963
Db      305 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 364
QY      1964 GGACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2023
Db      365 GGACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 424
QY      2024 GTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2083
Db      425 GTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 484
QY      2084 CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2143
Db      485 CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 544
QY      2144 AATTAAGAGCAAAAGTCATTAATTAATTTCTT 2174
Db      545 AATTAAGAGCAAAAGTCATTAATTTCTT 575

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RESULT 14
AAC86511
ID AAC86511 standard; DNA; 3017 BP.
XX AAC86511;
AC
XX
XX 19-MAR-2001 (first entry)
XX
DE DNA construct comprising a maize promoter and Agrobacterium ipt gene.
XX
XX temporal gene expression; spatial gene expression; plant seed;
XX cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
XX yield stability; tip kernel abortion; seed set; isopentenyl transferase;
XX ipt; ss.
XX Synthetic.
XX Zea mays.
OS Agrobacterium tumefaciens.
XX
XX WO200063401-A1.
XX
XX 26-OCT-2000.
XX
XX 13-APR-2000; 2000WO-US009943.
XX PF
XX 16-APR-1999; 99US-0129844P.
XX PR
XX (PION-) PIONEER HI-BRED INT INC.
XX PA
XX Haben JE, Zinselmeier C, Tomes D;
XX
XX WPI; 2000-672743/65.
DR
XX Novel recombinant DNA construct useful for producing transgenic plants
PT having enhanced levels of cytokinin expression, improved stress tolerance
XX and yield stability.
XX
XX Disclosure; Page 72-73; 76pp; English.
XX
XX The present sequence represents a recombinant DNA molecule of the
CC invention. It comprises, in this order, a maize promoter, an
CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize
CC terminator. The DNA molecules of the invention comprise a genetic
CC construct consisting of a promoter directing temporal and/or spatial gene
CC expression in plant seed operatively linked to a cytokinin modulating
CC gene. The recombinant DNA molecules are useful for producing fertile,
CC transgenic plants capable of regulated expression of a cytokinin
CC modulating gene in developing seeds. They are also useful for improving
CC stress tolerance and yield stability in plants. The preferential
CC expression of recombinant DNA molecules of the invention occurs about 14-
CC 25 days after pollination. The transgenic plants thus produced have
CC enhanced levels of cytokinin expression exhibit improved seed size,
CC decreased tip kernel abortion and increased seed set during unfavourable
CC environmental conditions
XX
XX Sequence 3017 BP; 865 A; 679 C; 622 G; 851 T; 0 U; 0 Other;

Query Match 16.9%; Score 536.4; DB 3; Length 3017;
Best Local Similarity 83.9%; Pred. No. 5.3e-81;
Matches 606; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 2178 ACCATGAGCCCGCATCTAATTTTGGTCACTTGCACAGAAAGACGACCGCAT 2237
DB 1404 AACAAATGATCTTCGCTTAATTTTGGTCACTTGCACAGAAAGACATCGATCGAT 1463
QY 2238 AGCTCTTGGCCACAGACAGAGGCTTCAGTCTCTTGGTGAATGGGTCATCGTGTCC 2297
DB 1464 AGCTCTTGGCCACAGACAGTCTCCAGTCTCTCGTGAATGGGTCATCGTGTCC 1523
QY 2298 TCAACTATCAACGCGAAGCGGAGCAGCAACAGTGGAAAGAACTGAAGGAGCGGCTCT 2357
DB 1524 TCAACTATCAACGCGAAGCGGAGCAGCAACAGTGGAAAGAACTGAAGGAGCGCTCT 1583

QY 2358 CTACCTTGATGATCGGCTCTGTGTGAGGGTATCATCGACCCCAAGCATCATATAG 2417
DB 1584 GTACCTTGATGATCGGCTCTGTGTGAGGGTATCATCGACCCCAAGCATCATATAG 1643
QY 2418 GCTGATCGAGGAGGTATATATCATGATGAGGCAACGCGGCTTATTTCTTGAAGAGATC 2477
DB 1644 GCTGATCGAGGAGGTATATATCATGATGAGGCAACGCGGCTTATTTCTTGAAGAGATC 1703
QY 2478 CACCTGCTTGTCTCACTGACATGCGCGGCAACAGCTATTGAGATGACAGATTTTGTGGCA 2537
DB 1704 TATCTGCTTGTCTCACTGACATGCGCGGCAACAGCTATTGAGATGACAGATTTTGTGGCA 1763
QY 2538 TATTATTGCGCAAGATTACCGGCAACAGGACCTTATGAAAGCGGCAAGCGCAAGT 2597
DB 1764 TATTATTGCGCAAGATTACCGGCAACAGGACCTTATGAAAGCGGCAAGCGCAAGT 1823
QY 2598 TAAGCAGATGTTACGCGGCTGAGGCGCATTCATATTCAAGATGTTGTTATCTTTG 2657
DB 1824 TAAGCAGATGTTACGCGGCTGAGGCGCATTCATATTCAAGATGTTGTTATCTTTG 1883
QY 2658 GAATGAACCTCGGCTGAGGCGCATTCATATTCAAGATGATGATGATGATGATGATG 2717
DB 1884 GAGGAGACCTCGGCTGAGGCGCATTCATATTCAAGATGATGATGATGATGATGATGATG 1943
QY 2718 GTTGTCTAGCCAGAACCATGATCAGGCGAGATATGCTATTGCAAGTTGACGCAATATGGA 2777
DB 1944 ATTTGCTACCCAGAACCATGATCAGGCGAGATATGCTATTGCAAGTTGACGCAATATGGA 2003
QY 2778 AGTAAAGTGAATTATGAGATGCTCAGAGATATTCATCATCGGCGCAACAGAAACA 2837
DB 2004 GAATTAATGATTTACGATATGCTCAGAGATATTCATCATCGGCGCAACAGAAACA 2063
QY 2838 GAAATTCCTCCCAAGTTAAACGAGCGCTTTGACGATTCGAAGTCAATCCGTTGGAT 2897
DB 2064 GAAATTCCTCCCAAGTTAAACGAGCGCTTTGACGATTCGAAGTCAATCCGTTGGAT 2123
QY 2898 GT 2899
DB 2124 GT 2125

RESULT 15
AAC86514
ID AAC86514 standard; DNA; 721 BP.
XX AAC86514;
AC
XX
XX 19-MAR-2001 (first entry)
XX
DE Nucleotide sequence of an isopentenyl transferase (ipt) gene fragment.
XX
XX temporal gene expression; spatial gene expression; plant seed;
XX cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
XX yield stability; tip kernel abortion; seed set; isopentenyl transferase;
XX ipt; ss.
XX
XX Agrobacterium tumefaciens.
XX
XX WO200063401-A1.
XX
XX 26-OCT-2000.
XX
XX 13-APR-2000; 2000WO-US009943.
XX PF
XX 16-APR-1999; 99US-0129844P.
XX PR
XX (PION-) PIONEER HI-BRED INT INC.
XX PA
XX Haben JE, Zinselmeier C, Tomes D;
XX
XX WPI; 2000-672743/65.
DR
XX Novel recombinant DNA construct useful for producing transgenic plants

PT having enhanced levels of cytokinin expression, improved stress tolerance
PT and yield stability.

XX
XX
PS Disclosure; Page 16; 76pp; English.

CC The present sequence represents an isopentenyl transferase gene fragment.
CC The fragment was used to produce the recombinant DNA molecules of the
CC invention. These comprise a genetic construct consisting of a promoter
CC directing temporal and/or spatial gene expression in plant seed
CC operatively linked to a cytokinin modulating gene. The recombinant DNA
CC molecules are useful for producing fertile, transgenic plants capable of
CC regulated expression of a cytokinin modulating gene in developing seeds.
CC They are also useful for improving stress tolerance and yield stability
CC in plants. The preferential expression of recombinant DNA molecules of
CC the invention occurs about 14-25 days after pollination. The transgenic
CC plants thus produced have enhanced levels of cytokinin expression exhibit
CC improved seed size, decreased tip kernel abortion and increased seed set
CC during unfavourable environmental conditions

XX
SQ Sequence 721 BP; 182 A; 176 C; 191 G; 172 T; 0 U; 0 Other;

Query Match 16.8%; Score 536; DB 3; Length 721;

Best Local Similarity 84.6%; Pred. No. 5.8e-81; Mismatches 110; Indels 0; Gaps 0;

Matches 602; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 2188 CTGCATCTAATTTTCGCTCACTTGCACAGAAAAGACGACCGGATAGCTTTGCC 2247

Db 8 CTAGCTCAATTTTCGCTCACTTGCACAGAAAAGACGACCTGCGATAGCTTTGCC 67

QY 2248 CAGCAGACAGGAGCTTCCAGTCTCTTCGTTGATGGGTCCTCAATCGTCTCACTATCA 2307

Db 68 CAGCAGACTGGCTCCCTCCAGTCTCTTCGTTGATGGGTCCTCAATCGTCTCACTATCA 127

QY 2308 ACCGGAAGCGGACGACCAAGTGGAGAGACTGAAAGGACGACGCTCTACCTTGAT 2367

Db 128 ACCGGAAGCGGACGACCAAGTGGAGAGACTGAAAGGACGACGCTCTACCTTGAT 187

QY 2368 GATCGGCTCTGTGGAGGGATATCATCGACGCAAGAGCTCATAGGCTGATCGAG 2427

Db 188 GATCGGCTCTGTGGAGGGATATCATCGACGCAAGAGCTCATAGGCTGATCGAG 247

QY 2428 GAGGTGTATATCATGAGGCGGAGGCTTATTTGAGGAGGATCCACCTGCTG 2487

Db 248 GAGGTGTATATCATGAGGCGGAGGCTTATTTGAGGAGGATCCACCTGCTG 307

QY 2488 CTCACTGATGAGCGGCAAGAGCTATGAGAGTGCAGATTTTCTTGCCATATATGCG 2547

Db 308 CTCACTGATGAGCGGCAAGAGCTATGAGAGTGCAGATTTTCTTGCCATATATGCG 367

QY 2548 CACAAGTTACCCGACCAAGAGACCTTCATGAAAGCGGCCCAAGGCAAGTTAAGCAATG 2607

Db 368 AAGCAAGTTAAGCAAGAGAGAGCTTCATGAGAGCTGCGCAAGACCAAGTTAAGCAATG 427

QY 2608 TTGCAACCCGCTGACAGGCGCATTTCTATATTCAGAGTTGGTTATCTTTGAAATGACCT 2667

Db 428 TTGCAACCCGCTGACAGGCGCATTTCTATATTCAGAGTTGGTTATCTTTGAAATGACCT 487

QY 2668 CGGCTGAGGCGCATTTCTGAAAGAGATCGATGATTCATGCAATGTTGTTGCTAGC 2727

Db 488 CGGCTGAGGCGCATTTCTGAAAGAGATCGATGATTCATGCAATGTTGTTGCTAGC 547

QY 2728 CAGAACCAATGACGCGCAGATATGCTATTTGACGCTTACGCAATATGGAAGTTAGTTG 2787

Db 548 CAGAACCAATGACGCGCAGATATGCTATTTGACGCTTACGCAATATGGAAGTTAGTTG 607

QY 2788 ATTAAAGGATGCTCAGAGATATTTCAATCCATGCGCGCAACAGGACAGAAATTCGCC 2847

Db 608 ATTAAAGGATGCTCAGAGATATTTCAATCCATGCGCGCAACAGGACAGAAATTCGCC 667

QY 2848 CAAGTTAAGCAGCGCTTTCAGACGATTCGAAGGTCAATCCGTTCCGAATGT 2899

Db 668 TTGGTGGGCGCAGACTGTGCAAGCGTTTGAAGACCAACATTTGCAATGT 719

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2004, 22:40:04 / Search time 249 Seconds
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Searched: 662709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/BACKFILES1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3183	100.0	3183	1	US-08-413-135-1
2	3171	99.6	3182	4	US-08-971-395-1
3	734.8	23.1	745	3	US-09-073-587-4
4	733.4	23.0	24595	6	5428147-1
5	709	22.3	709	1	US-08-413-135-2
6	709	22.3	709	4	US-08-971-395-2
7	569	17.9	613	4	US-09-545-244A-11
8	344.4	10.8	584	1	US-08-054-985-2
9	257.2	8.1	1829	1	US-07-966-187-17
10	257.2	8.1	1863	1	US-08-525-507-16
11	257.2	8.1	1863	2	US-08-475-427-9
12	257.2	8.1	1863	2	US-07-842-165-9
13	257.2	8.1	4284	1	US-08-525-507-14
14	256.2	8.0	15397	2	US-08-673-768-1
15	256.2	8.0	15397	2	US-08-673-768-1
16	256	8.0	2633	3	US-08-452-267-2
17	256	8.0	2633	3	US-09-123-644-2
18	256	8.0	5534	1	US-08-452-267-3
19	256	8.0	5534	3	US-09-123-644-3
20	255	8.0	6548	3	US-08-894-440-1
21	255	8.0	6548	3	US-08-817-188-2
22	255	8.0	6548	4	US-09-458-093-1
23	254.2	8.0	2709	4	US-09-319-275A-12
24	253.2	8.0	9299	4	US-09-097-319A-15
25	253.2	8.0	9335	4	US-09-097-319A-19
26	253.2	8.0	10160	4	US-09-097-319A-8
27	253.2	8.0	11784	4	US-09-097-319A-9

28	253.2	8.0	11991	4	US-09-097-319A-10	Sequence 10, Appl
29	253	7.9	2115	2	US-08-767-026-3	Sequence 3, Appl
30	253	7.9	2115	4	US-09-319-275A-3	Sequence 3, Appl
31	252.8	7.9	10249	4	US-09-186-002-14	Sequence 14, Appl
32	252.8	7.9	10252	4	US-09-186-002-15	Sequence 15, Appl
33	252.8	7.9	10339	4	US-09-186-002-13	Sequence 13, Appl
34	252.6	7.9	3237	2	US-08-419-075-26	Sequence 26, Appl
35	252.6	7.9	14194	4	US-09-577-424-3	Sequence 3, Appl
36	252.2	7.9	1138	4	US-09-011-151-8	Sequence 8, Appl
37	252.2	7.9	1138	4	US-09-011-151-9	Sequence 9, Appl
38	252.2	7.9	1630	4	US-09-441-340-23	Sequence 23, Appl
39	252.2	7.9	2378	4	US-09-441-340-27	Sequence 27, Appl
40	252.2	7.9	2436	4	US-09-441-340-31	Sequence 31, Appl
41	252.2	7.9	3754	4	US-09-377-466B-15	Sequence 15, Appl
42	252.2	7.9	4149	4	US-09-377-466B-13	Sequence 13, Appl
43	252.2	7.9	5592	4	US-09-495-797-37	Sequence 37, Appl
44	252.2	7.9	8349	4	US-09-186-002-16	Sequence 16, Appl
45	252.2	7.9	10846	4	US-09-098-219B-5	Sequence 5, Appl

ALIGNMENTS

```
RESULT 1
US-08-413-135-1
; Sequence 1, Application US/08413135
; Patent No. 5689042
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M
; APPLICANT: Gan, Suehang
; TITLE OF INVENTION: Transgenic Plants with Altered
; TITLE OF INVENTION: Senescence Characteristics
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413.135
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296.92808
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLSCULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SAG12-1 Promoter DNA"
;
; US-08-413-135-1
;
; Query Match 100.0%; Score 3183; DB 1; Length 3183;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 3183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GATATCTCTTTTATTAATCAATCAATAGATGATATGTTGAGAGAGCAACTATT 60
; DB 1 GATATCTCTTTTATTAATCAATCAATAGATGATGATGTTGAGAGAGCAACTATT 60
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QY	61	CTGTGAGCACCAGACTCTGTTTAAATATATGAAACCAGATTGTTATTTTAACTAGAC	120
Db	61	CTGTGAGCACCAGACTCTGTTTAAATATGAAACCAGATTGTTATTTTAACTAGAC	120
QY	121	AAAAAAGTAAATGCTGATGTTTAAATTTAAATAGTTGATCAGCTTGGATPAAA	180
Db	121	AAAAAAGTAAATGCTGATGTTTAAATTTAAATAGTTGATCAGCTTGGATPAAA	180
QY	181	AAATGATTAGTATCATAGCTAATATAGCATGATCTTAAATTTGTTTTGACACCTTT	240
Db	181	AAATGATTAGTATCATAGCTAATATAGCATGATCTTAAATTTGTTTTGACACCTTT	240
QY	241	TTTTCTCTCTTTGGTGTCTTTCTTACACTAGGAAGAACCCATAACATGACGTTCAAT	300
Db	241	TTTTCTCTCTTTGGTGTCTTTCTTACACTAGGAAGAACCCATAACATGACGTTCAAT	300
QY	301	AATTAAAAACAATTTTCCAAAGTTTATATACGAACTTGTTTTTAAATGAAAACAGT	360
Db	301	AATTAAAAACAATTTTCCAAAGTTTATATATACGAACTTGTTTTTAAATGAAAACAGT	360
QY	361	GAAATGTTGATTATGATTTAGTTAGATCAATACCTCAATATATGATCAATATGATATAT	420
Db	361	GAAATGTTGATTATGATTTAGTTAGATCAATACCTCAATATATGATCAATATGATATAT	420
QY	421	ATGAACCTCAGTTGTTATACAGAAATGAAATGCTATTTAAATACCCGATCATGAGTGTT	480
Db	421	ATGAACCTCAGTTGTTATACAGAAATGAAATGCTATTTAAATACCCGATCATGAGTGTT	480
QY	481	AAAAAGTGTCAATATGACATGAAAGCTTTTGTCCTACCGGGATATGAGTTAAGGTTT	540
Db	481	AAAAAGTGTCAATATGACATGAAAGCTTTTGTCCTACCGGGATATGAGTTAAGGTTT	540
QY	541	GGATCTCCAGAAATATTTGGGCCATTTAGTTATATTTGGGCTTAAAGCCTTTGGAAA	600
Db	541	GGATCTCCAGAAATATTTGGGCCATTTAGTTATATTTGGGCTTAAAGCCTTTGGAAA	600
QY	601	GAGACGAGGAAGAAAGATTGGGTCAAGTTAACAAAACAGACACTGATATTAGTTGGTA	660
Db	601	GAGACGAGGAAGAAAGATTGGGTCAAGTTAACAAAACAGACACTGATATTAGTTGGTA	660
QY	661	CTTTGGTAGCAGTGTGATTTATTTGGCCGATAAAACCTTGATACAACTGACAACTGTA	720
Db	661	CTTTGGTAGCAGTGTGATTTATTTGGCCGATAAAACCTTGATACAACTGACAACTGTA	720
QY	721	TGTTATTAGTTTGTACTGTGTGACCTTGGTTAGAAAAAGTGTATATATGTTAATCATCT	780
Db	721	TGTTATTAGTTTGTACTGTGTGACCTTGGTTAGAAAAAGTGTATATATGTTAATCATCT	780
QY	781	TGTGTTATGAGGTGATTTGTATTTATTTGTGACTAGGGGAGATTCCTTCAATCACA	840
Db	781	TGTGTTATGAGGTGATTTGTATTTATTTGTGACTAGGGGAGATTCCTTCAATCACA	840
QY	841	TAACAAAAGTTTATAGATTTTATTTTATACATTTTGGCAAGCTTGTGAAAGTTGGTA	900
Db	841	TAACAAAAGTTTATAGATTTTATTTTATACATTTTGGCAAGCTTGTGAAAGTTGGTA	900
QY	901	TTTACACCGCATTTTCCCTGTACAGAACTATATATTTATTTATATATCTCAAGTT	960
Db	901	TTTACACCGCATTTTCCCTGTACAGAACTATATATTTATTTATATATCTCAAGTT	960
QY	961	GACAAATATATGTTTAAAGTTTTTATACATTTTAAATACAGTGAAGATCCAGAA	1020
Db	961	GACAAATATATGTTTAAAGTTTTTATACATTTTAAATACAGTGAAGATCCAGAA	1020
QY	1021	TATGTTCTACTTCTTCTTGTGTAGAAAACTAATATATCATATATATATATATCT	1080
Db	1021	TATGTTCTACTTCTTCTTGTGTAGAAAACTAATATATCATATATATATATATCT	1080
QY	1081	AATCATATATATTTGTAAATATGAGATTTATGTGCAATTTGATTTAGATTTTAGACGG	1140
Db	1081	AATCATATATATTTGTAAATATGAGATTTATGTGCAATTTGATTTAGATTTTAGACGG	1140

QY	1141	TTATCACTTCAGCCAAATATGATTGGATTATTAAGTCCAAATGCAATTTGCAACGATATCC	1200
Db	1141	TTATCACTTCAGCCAAATATGATTGGATTATTAAGTCCAAATGCAATTTGCAACGATATCC	1200
QY	1201	CTCTGCGCTAATGATATTTTCAATATTTCTATATTAATCCCTAATCAAGAGCTACA	1260
Db	1201	CTCTGCGCTAATGATATTTTCAATATTTCTATATTAATCCCTAATCAAGAGCTACA	1260
QY	1261	TTTATTTGTATTTCTATATGACAGGGAACCTTTCATAGAGATTGATAGATGGAATTTGGT	1320
Db	1261	TTTATATTTGTATTTCTATATGACAGGGAACCTTTCATAGAGATTGATAGATGGAATTTGGT	1320
QY	1321	GGGAACATCATGGAACAGGAACCTTTTAGCAATCATATCCATTTATCTACGAAAGAAAT	1380
Db	1321	GGGAACATCATGGAACAGGAACCTTTTAGCAATCATATCCATTTATCTACGAAAGAAAT	1380
QY	1381	ACTTAGGCTAATGAAGTCACTTGTTGTGAATGACTATGATTTGTATCAAAATTAATTTAT	1440
Db	1381	ACTTAGGCTAATGAAGTCACTTGTTGTGAATGACTATGATTTGTATCAAAATTAATTTAT	1440
QY	1441	TTGTGCAATCATTTTTCTTTTTGATTTGATTAAGCTTTTAACCTTGACGAAATGCTTCT	1500
Db	1441	TTGTGCAATCATTTTTCTTTTTGATTTGATTAAGCTTTTAACCTTGACGAAATGCTTCT	1500
QY	1501	TGTGAATTAACAGAACTTTTGAATTCAACTATTTTGAATTGTGTGAAGAAACAAAAGAAAT	1560
Db	1501	TGTGAATTAACAGAACTTTTGAATTCAACTATTTTGAATTGTGTGAAGAAACAAAAGAAAT	1560
QY	1561	TGCTGTTTATATGATATGATTAATTTTGATGCAAGTAAGGTAACCTACGTAACAAGAA	1620
Db	1561	TGCTGTTTATATGATATGATTAATTTTGATGCAAGTAAGGTAACCTACGTAACAAGAA	1620
QY	1621	AAATTAACATGTAGCTAATCACTACGTATCAGCATGTAAAGTAATTTTTTCCAAATTAATTA	1680
Db	1621	AAATTAACATGTAGCTAATCACTACGTATCAGCATGTAAAGTAATTTTTTCCAAATTAATTA	1680
QY	1681	TACTCANGATATTTTTTTTTTTTGAATGTCAATTAATAATGCTTCTTAAATATTA	1740
Db	1681	TACTCANGATATTTTTTTTTTTTGAATGTCAATTAATAATGCTTCTTAAATATTA	1740
QY	1741	TTTTTAATTAATTAATAAGAAATATATTTATGAAATCAATCATCAACATATCCAACT	1800
Db	1741	TTTTTAATTAATTAATAAGAAATATATTTATGAAATCAATCATCAACATATCCAACT	1800
QY	1801	TGGAATATCTCTATATGTAACAGATGAGAAATTAATTTTACTAGATACAAACTTCTTA	1860
Db	1801	TGGAATATCTCTATATGTAACAGATGAGAAATTAATTTTACTAGATACAAACTTCTTA	1860
QY	1861	ATCATCATATTAATAATGTTTACAAATCTAATTAACCAACCAACATTAATTAACCTAAAT	1920
Db	1861	ATCATCATATTAATAATGTTTACAAATCTAATTAACCAACCAACATTAATTAACCTAAAT	1920
QY	1921	CCGAGCAAGTGAAGTAACAAGACTGATTTCAAGTTGATGTAGAGACTAAATGGCTACG	1980
Db	1921	CCGAGCAAGTGAAGTAACAAGACTGATTTCAAGTTGATGTAGAGACTAAATGGCTACG	1980
QY	1981	TATCAAAACATCAACGATCATTTAGTATGATATGATGATGATGATGATCATTACTTGTAAC	2040
Db	1981	TATCAAAACATCAACGATCATTTAGTATGATATGATGATGATGATGATGATCATTACTTGTAAC	2040
QY	2041	AAAAATGCTTGAATTTGGATCATCACTTCATCTGTAACATTAAGCAATTAACATCAACCTTA	2100
Db	2041	AAAAATGCTTGAATTTGGATCATCACTTCATCTGTAACATTAAGCAATTAACATCAACCTTA	2100
QY	2101	TTTTTCTATAAACCCTCATCTCAATACCCCTCTCAAGTAATCAAAATTAAGCAAAAGT	2160
Db	2101	TTTTTCTATAAACCCTCATCTCAATACCCCTCTCAAGTAATCAAAATTAAGCAAAAGT	2160
QY	2161	CATTTAATCTTCTATAAACCATGAGACCTGCAATCTAATTTTGGTCAACTTGCACAGGA	2220
Db	2161	CATTTAATCTTCTATAAACCATGAGACCTGCAATCTAATTTTGGTCAACTTGCACAGGA	2220
QY	2221	AAGACGACGACCGGATAGCTCTTGCCACGACAGACAGGCTTCCAGTCTCTTGTTAT	2280

2221 AAGACGACGACCGGATAGCTCTGCCCAGACAGAGGCTTCCAGTCTTGGCTTAT 2280
 2281 CGGGTCCATCGTGTCTCAACTATCAACGGAAGCGGACGACCAAGATGGAAGACTG 2340
 2281 CGGGTCCATCGTGTCTCAACTATCAACGGAAGCGGACGACCAAGATGGAAGACTG 2340
 2341 AAGAGAACGAGCGCTCTCACTGATGATGATGATGATGATGATGATGATGATGATG 2400
 2341 AAGAGAACGAGCGCTCTCACTGATGATGATGATGATGATGATGATGATGATGATG 2400
 2401 AAGAGAACGATCATAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 2460
 2401 AAGAGAACGATCATAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 2460
 2461 ATTCTTGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520
 2461 ATTCTTGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520
 2521 GACAGATTTTGGTGGCATATTTATTTGCGCAGATTTACCCGACCAAGAGACCTTCA 2580
 2521 GACAGATTTTGGTGGCATATTTATTTGCGCAGATTTACCCGACCAAGAGACCTTCA 2580
 2581 GCGGCGCAAGGCGCAAGATTTAGCAGATTTGACACCCCGCTGACGACCATTTATTTCA 2640
 2581 GCGGCGCAAGGCGCAAGATTTAGCAGATTTGACACCCCGCTGACGACCATTTATTTCA 2640
 2641 GAGTTGGTTTATCTTTGGAATGAACCTGCGTGGAGGCGGCTTGAAGAGATGATGATG 2700
 2641 GAGTTGGTTTATCTTTGGAATGAACCTGCGTGGAGGCGGCTTGAAGAGATGATGATG 2700
 2701 TATGATATGCGCATGTTGTTGCTAGCCAGAACGATCAGGCGAGATATCTATTTGAG 2760
 2701 TATGATATGCGCATGTTGTTGCTAGCCAGAACGATCAGGCGAGATATCTATTTGAG 2760
 2761 CTGACGCAAAATATGGAAGATGATGATGATGATGATGATGATGATGATGATGATG 2820
 2761 CTGACGCAAAATATGGAAGATGATGATGATGATGATGATGATGATGATGATGATG 2820
 2821 GCGGCGCAAGGCGCAAGATTTCCCGCAAGTTAAGGACGCGCTTGAAGAGATGATG 2880
 2821 GCGGCGCAAGGCGCAAGATTTCCCGCAAGTTAAGGACGCGCTTGAAGAGATGATG 2880
 2881 GGTATCCGTTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940
 2881 GGTATCCGTTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940
 2941 GGCATATAAGTTCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
 2941 GGCATATAAGTTCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
 3001 TTCTGTGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060
 3001 TTCTGTGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3060
 3061 GATGGGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
 3061 GATGGGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120
 3121 TATGGCGGCAAGGCGGATTAATGATGATGATGATGATGATGATGATGATGATGATG 3180
 3121 TATGGCGGCAAGGCGGATTAATGATGATGATGATGATGATGATGATGATGATGATG 3180
 3181 TTC 3183
 3181 TTC 3183

RESULT 2
 US-08-971-395-1
 ; Sequence 1, Application US/08971395
 ; Patent No. 6359197
 ; GENERAL INFORMATION:

APPLICANT: Amasino, Richard M
 APPLICANT: No. 6359197, Yoo-Sun
 APPLICANT: Gan, Susheeng
 TITLE OF INVENTION: Transgenic Plants with Altered
 TITLE OF INVENTION: Transgenic Plants with Altered
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinekey Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/971,395
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27386
 REFERENCE/DOCKET NUMBER: 960296.94908
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-251-5000
 TELEFAX: 608-251-9166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3182 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-971-395-1

Query Match 99.6%; Score 3171; DB 4; Length 3182;
 Best local similarity 100.0%; Pred. No. 0;
 Matches 3182; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 1 GATATCTTTTATTTATTTCAAGATAGTGAATATGTTGAGAGAGCAACTAT 60
 1 GATATCTTTTATTTATTTCAAGATAGTGAATATGTTGAGAGAGCAACTAT 60
 61 CTCGTGAGACGACGATCTGTTTATATTTAGAAACCGGATGTTATTTAGACTGAC 120
 61 CTCGTGAGACGACGATCTGTTTATATTTAGAAACCGGATGTTATTTAGACTGAC 120
 121 AAAAAAGTAATCGTGAATGTTAAATTTAAATTTAGTTTCACTGATGATGAT 180
 121 AAAAAAGTAATCGTGAATGTTAAATTTAAATTTAGTTTCACTGATGATGATGAT 180
 121 AAAAAAGTAATCGTGAATGTTAAATTTAAATTTAGTTTCACTGATGATGATGAT 180
 181 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 181 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 241 TTTCTCTCTTGGTGTGTTTCTTAACATTAGAGAACCCATPAACATGATGATGAT 300
 241 TTTCTCTCTTGGTGTGTTTCTTAACATTAGAGAACCCATPAACATGATGATGATGAT 300
 301 AATTAATAACAATATTTTCAAGTTTATATATGAAACCTGTTTATATGAAACAGTT 360
 301 AATTAATAACAATATTTTCAAGTTTATATATGAAACCTGTTTATATGAAACAGTT 360
 301 AATTAATAACAATATTTTCAAGTTTATATATGAAACCTGTTTATATGAAACAGTT 360
 361 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 361 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 421 ATGAACCTAGTTGTTATCAAGAAATGAAATGCTATTTAAATACGATCATGAGTGT 480
 421 ATGAACCTAGTTGTTATCAAGAAATGAAATGCTATTTAAATACGATCATGAGTGT 480

QY 481 AAAAGTGCAGAAATGACATGAGGCTTTTGTCCATCCGGGTATGAGTT 540
Db 481 AAAAGTGCAGAAATGACATGAGGCTTTTGTCCATCCGGGTATGAGTT 540
QY 541 GGAATCTCAGAAATATTTGGGCGATTAATAGTATATTTGGGCTTAAGGTTTGCAA 600
Db 541 GGAATCTCAGAAATATTTGGGCGATTAATAGTATATTTGGGCTTAAGGTTTGCAA 600
QY 601 GAGACGAGAGAAAGATGGGTCAAGTTAAACAAACAGAGACCTCGATTAAGTTGTA 660
Db 601 GAGACGAGAGAAAGATGGGTCAAGTTAAACAAACAGAGACCTCGATTAAGTTGTA 660
QY 661 CTGTGTAGCAAGTCGATTTATTTGCCAGTAAACCTTGGTACAACTGACAACTGTA 720
Db 661 CTGTGTAGCAAGTCGATTTATTTGCCAGTAAACCTTGGTACAACTGACAACTGTA 720
QY 721 TCGTATTAAGTTGTGACTGTGGTACCTTGGTAAAGAAAGTTGATTAAGTTAAGT 780
Db 721 TCGTATTAAGTTGTGACTGTGGTACCTTGGTAAAGAAAGTTGATTAAGTTAAGT 780
QY 781 TGTGTGATGAGTGTGATTTAAATTTGTGACTAGGCGGATTCCTTCACTCAACAA 840
Db 781 TGTGTGATGAGGATTTGATTTAAATTTGTGACTAGGCGGATTCCTTCACTCAACAA 840
QY 841 TAAACAAGTTTATGATTTTATTTATTAACATTTTGGCCGCTTGGTAAAGTTGTA 900
Db 841 TAAACAAGTTTATGATTTTATTTATTAACATTTTGGCCGCTTGGTAAAGTTGTA 900
QY 901 TTTTACACCGCATTTTCCCTGTACAGAAATCATATATTTATTTATTAATCTCACT 960
Db 901 TTTTACACCGCATTTTCCCTGTACAGAAATCATATATTTATTTATTAATCTCACT 960
QY 901 TTTTACACCGCATTTTCCCTGTACAGAAATCATATATTTATTTATTAATCTCACT 960
Db 901 TTTTACACCGCATTTTCCCTGTACAGAAATCATATATTTATTTATTAATCTCACT 960
QY 961 GACATTTAAGTTAATGATTTTACATTTTAAACATGTAAGTCAAGTCAAGAA 1020
Db 961 GACATTTAAGTTAATGATTTTACATTTTAAACATGTAAGTCAAGTCAAGAA 1020
QY 1021 TATGTCTTACTTCTTCTTGTGTAGAAACCTAATATGATTAATTAATTTCT 1080
Db 1021 TATGTCTTACTTCTTCTTGTGTAGAAACCTAATATGATTAATTAATTTCT 1080
QY 1081 AATCATTTAATTTGAAATATGACAGTATTTGCAATTTGATTTAGTTTAAAGCG 1140
Db 1081 AATCATTTAATTTGAAATATGACAGTATTTGCAATTTGATTTAGTTTAAAGCG 1140
QY 1141 TTAATCACTTACGCAAAATATGATTTGATTAAGTCAAAATGCAATTTGTAAGTCC 1200
Db 1141 TTAATCACTTACGCAAAATATGATTTGATTAAGTCAAAATGCAATTTGTAAGTCC 1200
QY 1201 CTCTGTGTCTAATGATTTATTTCAATTTCTTATTTATTTCCCTTAACAGAGCTCA 1260
Db 1201 CTCTGTGTCTAATGATTTATTTCAATTTCTTATTTATTTCCCTTAACAGAGCTCA 1260
QY 1261 TTTATTTGATTTCTATATGACAGGAACTTTCAATGAGTTCAAGTAAATTTGGT 1320
Db 1261 TTTATTTGATTTCTATATGACAGGAACTTTCAATGAGTTCAAGTAAATTTGGT 1320
QY 1321 GGGAAACATCATTTGAACAGAAACCTTTAGCAAAATCATTCATTTATTTCAAAAGAT 1380
Db 1321 GGGAAACATCATTTGAACAGAAACCTTTAGCAAAATCATTCATTTATTTCAAAAGAT 1380
QY 1381 ACTTACCGTAAAGATTTCACTTGTGTGAATGACATGATTTGATTTAGTTAAT 1440
Db 1381 ACTTACCGTAAAGATTTCACTTGTGTGAATGACATGATTTGATTTAGTTAAT 1440
QY 1441 TGTGCAATCATTTTCTTTTGAATTTGATTAAGCTTTTAACTTGACAGATTTCTCT 1500
Db 1441 TGTGCAATCATTTTCTTTTGAATTTGATTTAGTTAAGCTTTTAACTTGACAGATTTCTCT 1500
QY 1501 TGTGAATTAACAGAACTTTTGAATTTCAACTATTTATTTAGTAAAGCAAAAGAGAT 1560
Db 1501 TGTGAATTAACAGAACTTTTGAATTTCAACTATTTATTTAGTAAAGCAAAAGAGAT 1560

QY 1561 TCCCTGTTTATGATTAAGTATTTGATTTGATTCATGAAAGTACCTTACTTACAGAA 1620
Db 1561 TCCCTGTTTATGATTAAGTATTTGATTTGATTCATGAAAGTACCTTACTTACAGAA 1620
QY 1621 AAATAAATGATGATTTACTTACATGATTCAGATGATTAAGTATTTTCCAAATTTA 1680
Db 1621 AAATAAATGATGATTTACTTACATGATTCAGATGATTAAGTATTTTCCAAATTTA 1680
QY 1681 TACTCATGATTAATTTTGTGAAATGCAATTAATAAAGTCTTCTTAATTTA 1740
Db 1681 TACTCATGATTAATTTTGTGAAATGCAATTAATAAAGTCTTCTTAATTTA 1740
QY 1741 TTTTAAATTAATTAAGAAATATTTATTTAGCAAAATCATTCACATTTCAACT 1800
Db 1741 TTTTAAATTAATTAAGAAATATTTATTTAGCAAAATCATTCACATTTCAACT 1800
QY 1801 TCGAAATCTCTATGATTAAGCAAGTGAAGAAATTAATTTTACTAGATCAAACTTCTA 1860
Db 1801 TCGAAATCTCTATGATTAAGCAAGTGAAGAAATTAATTTTACTAGATCAAACTTCTA 1860
QY 1861 ATCATGATTAATTAATTTTAACTTAACCACTTAATTAATTTAATTTAAT 1920
Db 1861 ATCATGATTAATTAATTTTAACTTAACCACTTAATTAATTTAATTTAAT 1920
QY 1921 CCGAGCAAGTGAAGTGAACAGACTTGAATTCAGTTGATGATTAAGTAAATGCTTAC 1980
Db 1921 CCGAGCAAGTGAAGTGAACAGACTTGAATTCAGTTGATGATTAAGTAAATGCTTAC 1980
QY 1981 TATCAAAATCAACGATCATTTGATTAAGTAAATGATTAAGTAAATGCTTAC 2040
Db 1981 TATCAAAATCAACGATCATTTGATTAAGTAAATGATTAAGTAAATGCTTAC 2040
QY 2041 AAATAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2100
Db 2041 AAATAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 2100
QY 2101 TTTTCACTTAAACCCCATCTGATGATTCCTTCTGAAATTAATCAATTAAGTAAAGT 2160
Db 2101 TTTTCACTTAAACCCCATCTGATGATTCCTTCTGAAATTAATCAATTAAGTAAAGT 2160
QY 2161 CATTTAATTTTCCCTTAACCAATGAGACCTGATTAATTTTCCCTTCACTTGAACAGA 2220
Db 2161 CATTTAATTTTCCCTTAACCAATGAGACCTGATTAATTTTCCCTTCACTTGAACAGA 2220
QY 2221 AAGACGAGACCGGATGATCTTGGCCAGAGACAGGCTTCCAGTCTTCTGAT 2280
Db 2221 AAGACGAGACCGGATGATCTTGGCCAGAGACAGGCTTCCAGTCTTCTGAT 2280
QY 2281 CGGATCAATGATGCTTCAATCAATCAACCGGAACCGGACCAACAGTGAAGAGATG 2340
Db 2281 CGGATCAATGATGCTTCAATCAATCAACCGGAACCGGACCAACAGTGAAGAGATG 2340
QY 2341 AAAGAAACGAGCGCTCTAATGATTAAGTGGCTGATGAGGATGATGATGATGATGATG 2400
Db 2341 AAAGAAACGAGCGCTCTAATGATTAAGTGGCTGATGAGGATGATGATGATGATGATG 2400
QY 2401 AAGCAAGCTCATTAAGCTGATGAGAGGATTAATCAATGAGGCAACGCGGCTT 2460
Db 2401 AAGCAAGCTCATTAAGCTGATGAGAGGATTAATCAATGAGGCAACGCGGCTT 2460
QY 2460 ATTTTGAAGGAGATCACTCTGTTGCTCAATGCAATGAGCGGCAACGCTTATGAGT 2520
Db 2460 ATTTTGAAGGAGATCACTCTGTTGCTCAATGCAATGAGCGGCAACGCTTATGAGT 2520
QY 2521 GCAATTTTCTGTTGCAATTAATTTGCAACAGTAACTTCCAGCAAGAGCTTCAAGAA 2580
Db 2521 GCAATTTTCTGTTGCAATTAATTTGCAACAGTAACTTCCAGCAAGAGCTTCAAGAA 2580
QY 2581 GCGGCAAGGCGAGATTAAGCAAGTGTGACCCCGCTGACAGGCTTCTATTTATGCA 2640
Db 2581 GCGGCAAGGCGAGATTAAGCAAGTGTGACCCCGCTGACAGGCTTCTATTTATGCA 2640
QY 2641 GAGTTGTTATCTTTGGAATGAACCTGCGCTGAGGCGCATTTCTGAAGAGATGATGGA 2700
Db 2641 GAGTTGTTATCTTTGGAATGAACCTGCGCTGAGGCGCATTTCTGAAGAGATGATGGA 2700

Db 2640 GAGTTGGTTATCTTTGGAAAGAACTTCGCTGAGGCCCATCTTGAAGAGATGATGGA 2639
Qy 2701 TATGATATGCGCATGTTGTTGTTAGTACGAGAACAGATCAGGAGATATGCTATTGAG 2760
Db 2700 TATGATATGCGCATGTTGTTGTTAGTACGAGAACAGATCAGGAGATATGCTATTGAG 2759
Qy 2761 CTGACGCAATATGAGAGGTAAGTTGATTAATGAGATCGCTCAGAGATATTCATCCAT 2820
Db 2760 CTGACGCAATATGAGAGGTAAGTTGATTAATGAGATCGCTCAGAGATATTCATCCAT 2819
Qy 2821 GCGGCGCCAGACGAGAACGAAATTCCTCCAGATTAACGAGCGCTTCGAGAGATTCGAA 2880
Db 2820 GCGGCGCCAGACGAGAACGAAATTCCTCCAGATTAACGAGCGCTTCGAGAGATTCGAA 2879
Qy 2881 GGTATCCGCTGCGAATATATTAAGTTACGCGAGCCCTGAGCTGATCGTCAACAATTT 2940
Db 2880 GGTATCCGCTGCGAATATATTAAGTTACGCGAGCCCTGAGCTGATCGTCAACAATTT 2939
Qy 2941 GGCATAAAGTTTCTTAAGATTGAATCCTGTGCGCGGTCTTGCGAGATTAATCAATATAT 3000
Db 2940 GGCATAAAGTTTCTTAAGATTGAATCCTGTGCGCGGTCTTGCGAGATTAATCAATATAT 2999
Qy 3001 TTCTGTTGAATTAAGTTAGATTAAGATTAATTAATTAATTAATTAATTAATTAATTAAT 3060
Db 3000 TTCTGTTGAATTAAGTTAGATTAAGATTAATTAATTAATTAATTAATTAATTAATTAAT 3059
Qy 3061 GATGGGTTTTATGATTAAGTCCCGCAATTATACATTAAATAGCGATAGAAAACAAA 3120
Db 3060 GATGGGTTTTATGATTAAGTCCCGCAATTATACATTAAATAGCGATAGAAAACAAA 3119
Qy 3121 TATGCGCGCAACCTGGATTAATTAATGCGCGCGGTCTATGTTACTAGATCGAA 3180
Db 3120 TATGCGCGCAACCTGGATTAATTAATGCGCGCGGTCTATGTTACTAGATCGAA 3179
Qy 3181 TTC 3183
Db 3180 TTC 3182

RESULT 3
US-09-073-587-4
Sequence 4, Application US/09073587
Patent No. 6268552
GENERAL INFORMATION:
APPLICANT: L.I. YI
TITLE OF INVENTION: Transgenic Seedless Plants
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,587
FILING DATE: 06-MAY-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,725
FILING DATE: 06-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 4-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..725
US-09-073-587-4

Query Match 23.1%; Score 734.8; DB 3; Length 745;
Best Local Similarity 99.7%; Pred. No. 3.2e-151;
Matches 736; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2187 CTTGATCTTAATTTTTCGCTTCAACTTGGACAGGAAAGACGACCGGATAGCTTTGC 2246
Db 8 CTTGATCTTAATTTTTCGCTTCAACTTGGACAGGAAAGACGACCGGATAGCTTTGC 67
Qy 2247 CCAGCAGACGAGGCTTCCAGTCTTTGCTTGAATCGGGTCCAAATCGTCTCCCAATC 2306
Db 68 CCAGCAGACGAGGCTTCCAGTCTTTGCTTGAATCGGGTCCAAATCGTCTCCCAATC 127
Qy 2307 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAGAAAGACGCGCTCTTACCTTGA 2366
Db 128 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAGAAAGACGCGCTCTTACCTTGA 187
Qy 2367 TGATCGGCTCTGCTGAGAGGATATCATTCGACGCCAAGCACTCATATAGGCTGATGA 2426
Db 188 TGATCGGCTCTGCTGAGAGGATATCATTCGACGCCAAGCACTCATATAGGCTGATGA 247
Qy 2427 GAGGTGATATATCATGAGGCAACGCGGCTTATTTCTGAGGAGATCACTCGTT 2486
Db 248 GAGGTGATATATCATGAGGCAACGCGGCTTATTTCTGAGGAGATCACTCGTT 307
Qy 2487 GCTCACTGATGCGCGGAAACAGCTATTTGAGATGCAATTTTGTGGCATATATTCG 2546
Db 308 GCTCACTGATGCGCGGAAACAGCTATTTGAGATGCAATTTTGTGGCATATATTCG 367
Qy 2547 CCAGATGTTACCGACCAAGAGACCTTCATGAAGCGGCCAAGGCGCAGATTAAGCAGAT 2606
Db 368 CCAGATGTTACCGACCAAGAGACCTTCATGAAGCGGCCAAGGCGCAGATTAAGCAGAT 427
Qy 2607 GTTGCAACCCGCTGACGCGCATTTCTATTTCAAGAGTTGTTATCTTTGGAATGAACC 2666
Db 428 GTTGCAACCCGCTGACGCGCATTTCTATTTCAAGAGTTGTTATCTTTGGAATGAACC 487
Qy 2667 TCGGCTGAGGCCCATTTCTGAAGAGATGATGATATGATATGATGATGATGATGATGATG 2726
Db 488 TCGGCTGAGGCCCATTTCTGAAGAGATGATGATATGATGATGATGATGATGATGATGATG 547
Qy 2727 CCAGAACGAGATCAACGAGATATGCTATTTGAGCTTACCGCAATATGAGAGTAACTT 2786
Db 548 CCAGAACGAGATCAACGAGATATGCTATTTGAGCTTACCGCAATATGAGAGTAACTT 607
Qy 2787 GATTATGAGATCGCTCAGAGATATTTTCATCCATCGCGCCCAACGAGAACGAAATTCCT 2846
Db 608 GATTATGAGATCGCTCAGAGATATTTTCATCCATCGCGCCCAACGAGAACGAAATTCCT 667
Qy 2847 CCAAGTTAACGAGCGCTTTTCGAGAGATGGAAGTATCCGTTCCGAATGATTAAGT 2906
Db 668 CCAAGTTAACGAGCGCTTTTCGAGAGATGGAAGTATCCGTTCCGAATGATTAAGT 727
Qy 2907 TAAGCCAGCCCTGAGCTC 2924
Db 728 TAAGCCAGCCCTGAGCTC 745

RESULT 4

5428147-1
Patent No. 5428147
APPLICANT: BARKER, RICHARD F.; KEMP, JOHN D.
TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/91,538
FILING DATE: 13-JUL-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 869,216
FILING DATE: 13-APR-1992
APPLICATION NUMBER: 869,216
FILING DATE: 13-APR-1992
APPLICATION NUMBER: 440,432
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 553,786
FILING DATE: 19-NOV-1983
APPLICATION NUMBER: 741,034
FILING DATE: 06-AUG-1991
APPLICATION NUMBER: 144,775
FILING DATE: 20-JAN-1988
APPLICATION NUMBER: 485,614
FILING DATE: 15-APR-1983
APPLICATION NUMBER: 713,624
FILING DATE: 10-JUN-1991
APPLICATION NUMBER: 260,574
FILING DATE: 21-OCT-1988
APPLICATION NUMBER: 848,733
FILING DATE: 01-APR-1986
APPLICATION NUMBER: 535,354
FILING DATE: 26-SEP-1983
SEQ ID NO: 1
LENGTH: 24595
5428147-1
Query Match 23.0%; Score 733.4; DB 6; Length 24595;
Best Local Similarity 96.0%; Pred. No. 1.8e-150;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 2139 TAAATCAATTAAGACAAAGTCAATTTAACTTCTTAAACCATGAGACCTGATCTAT 2198
DB 8728 TAAATCAATTAAGACAAAGTCAATTTAACTTCTTAAACCATGAGACCTGATCTAT 8787
QY 2139 TTTGGTCCAACTTGACAGAAAGACGACGCGGATGCTTTGCCAGACACGCG 2258
DB 8788 TTTGGTCCAACTTGACAGAAAGACGACGCGGATGCTTTGCCAGACACGCG 8847
QY 2259 GCTTCAGTCTTTGGCTTGTATCGGCTCAATCGTGTCTCAATCAATCAACCGAAGCGG 2318
DB 8848 GCTTCAGTCTTTGGCTTGTATCGGCTCAATCGTGTCTCAATCAATCAACCGAAGCGG 8907
QY 2319 ACACCAACAGTGAAGAACTGAAGAAAGACGACGCGTCTCTAACCCTTGATGATCGGCTCT 2378
DB 8908 ACACCAACAGTGAAGAACTGAAGAAAGACGACGCGTCTCTAACCCTTGATGATCGGCTCT 8967
QY 2379 GGTGAGGATATCATGACGACCAAGCAAGCTATCATTAAGGCTGATGAGAGAGTGTATTA 2438
DB 8968 GGTGAGGATATCATGACGACCAAGCAAGCTATCATTAAGGCTGATGAGAGAGTGTATTA 9027
QY 2439 TATAGGAGCAACGCGGCGCTTATTTGAGGAGAGATCACTCGTGTCTCAACTGCAT 2498
DB 9028 TATAGGAGCAACGCGGCGCTTATTTGAGGAGAGATCACTCGTGTCTCAACTGCAT 9087
QY 2499 GGGGCAACAGCTATTTGAGAGTGCAGATTTTGGTGGCATATTAATCGCCACAAGTTACC 2558
DB 9088 GGGGCAACAGCTATTTGAGAGTGCAGATTTTGGTGGCATATTAATCGCCACAAGTTACC 9147
QY 2559 CGACCAAGAGACTTATGAAAGCGCCCAAGGCAAGATTAAGACAGATTTGACACCCCGC 2618
DB 9148 CGACCAAGAGACTTATGAAAGCGCCCAAGGCAAGATTAAGACAGATTTGACACCCCGC 9207
QY 2619 TGGAGGCACTTCAATTAATCAAGATTTGTTTCTTTGGATGAAGCTCGGCTGAGGCC 2678

DB 9208 TCGAGGCACTTCTATTAATCAAGATTTGTTTAACTTTGGAATGAACCTCGGCTGAGGCC 9267
QY 2679 CATTCTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2738
DB 9268 CATTCTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9327
QY 2739 CACGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2798
DB 9328 CACGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9387
QY 2799 CGCTCAGAGATATTTCAATCCATGCGCGCAACAGAAAGATTTCCCAAGTTAACGC 2858
DB 9388 CGCTCAGAGATATTTCAATCCATGCGCGCAACAGAAAGATTTCCCAAGTTAACGC 9447
QY 2859 AGCCGCTTTGACAGATTTGAAAGTCAATCGCTTGGAAATGATTAAGGTAACGCGCT 2918
DB 9448 AGCCGCTTTGACAGATTTGAAAGTCAATCGCTTGGAAATGATTAAGGTAACGCGCT 9507
QY 2919 GAG 2921
DB 9508 GCG 9510

RESULT 5

US-08-413-135-2

Sequence 2, Application US/08413135

Patent No. 5689042

GENERAL INFORMATION:

APPLICANT: Amasino, Richard M

TITLE OF INVENTION: Transgenic Plants with Altered

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53703

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/413,135

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J

REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 960296, 92808

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 709 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "SAG12-1 Promoter DNA

DESCRIPTION: (truncated)"

US-08-413-135-2

Query Match 22.3%; Score 709; DB 1; Length 709;
Best Local Similarity 100.0%; Pred. No. 1.3e-145;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1472 AAGCTTTTACTGACAGATGCTTCTTTGGAATTAACAGATTTGAATTAATCAACT 1531

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Db 1 AAGCTTTAACTTGACAGAAATGTTCTCTTGTAATAACAGAACTTTGAATCAAACT 60
Qy 1532 ATTGATTAGTGAAGAAAGCAAAAGAGATTCCTGTTTATGATTTAGATTTGAT 1591
Db 61 ATTGATTAGTGAAGAAAGCAAAAGAGATTCCTGTTTATGATTTAGATTTGAT 120
Qy 1592 GCATGAAGAGTACTACTACTACTACAGAAATTAACATGACGTAATCTAGTCAGCA 1651
Db 121 GCATGAAGAGTACTACTACTACTACAGAAATTAACATGACGTAATCTAGTCAGCA 180
Qy 1652 TGTAAAGATATTTTTCCTCAATATATTAATGATGATGATTTTTCCTGAAATG 1711
Db 181 TGTAAAGATATTTTTCCTCAATATATTAATGATGATGATTTTTCCTGAAATG 240
Qy 1712 TCAATTTAAAAATGCTTTCTTAATATTAATTTATTAATTAATTAAGAAATATATTTA 1771
Db 241 TCAATTTAAAAATGCTTTCTTAATATTAATTTATTAATTAATTAAGAAATATATTTA 300
Qy 1772 TGCAAAAATCATCATCAACATATCCAACTTGAAATCTCTATGTCACAGAGTAGAA 1831
Db 301 TGCAAAAATCATCATCAACATATCCAACTTGAAATCTCTATGTCACAGAGTAGAA 360
Qy 1832 AATAAATTTTACTAGATCAAAATCTCTAATCATCATTAATTAATGTTTACAAAATCTAAT 1891
Db 361 AATAAATTTTACTAGATCAAAATCTCTAATCATCATTAATTAATGTTTACAAAATCTAAT 420
Qy 1892 TAAACCCACCTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1951
Db 421 TAAACCCACCTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
Qy 1952 CAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2011
Db 481 CAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Qy 2012 TCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2071
Db 541 TCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Qy 2072 TGTGAACATTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2131
Db 601 TGTGAACATTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
Qy 2132 TGTGAACATTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2180
Db 661 TGTGAACATTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 709

RESULT 6
US-08-971-395-2
; Sequence 2, Application US/08971395
; Patent No. 6359197
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M
; APPLICANT: No. 6359197, Yoo-Sun
; APPLICANT: Gan, Susheng
; TITLE OF INVENTION: Transgenic Plants with Altered
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971.395
; FILING DATE:
```

```
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296, 94908
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-9166
TELEFAX: 608-251-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-971-395-2

Query Match 22.3%; Score 709; DB 4; Length 709;
Best Local Similarity 100.0%; Pred. No. 1,3e-145;
Matches 709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1472 AAGCTTTAACTTGACAGAAATGTTCTCTTGTAATAACAGAACTTTGAATCAAACT 1531
Db 1 AAGCTTTAACTTGACAGAAATGTTCTCTTGTAATAACAGAACTTTGAATCAAACT 60
Qy 1532 ATTGATTAGTGAAGAAAGCAAAAGAGATTCCTGTTTATGATTTAGATTTGAT 1591
Db 61 ATTGATTAGTGAAGAAAGCAAAAGAGATTCCTGTTTATGATTTAGATTTGAT 120
Qy 1592 GCATGAAGAGTACTACTACTACTACAGAAATTAACATGACGTAATCTAGTCAGCA 1651
Db 121 GCATGAAGAGTACTACTACTACTACAGAAATTAACATGACGTAATCTAGTCAGCA 180
Qy 1652 TGTAAAGATATTTTTCCTCAATATATTAATGATGATGATTTTTCCTGAAATG 1711
Db 181 TGTAAAGATATTTTTCCTCAATATATTAATGATGATGATTTTTCCTGAAATG 240
Qy 1712 TCAATTTAAAAATGCTTTCTTAATATTAATTTATTAATTAATTAATTAATTAATTAAT 1771
Db 241 TCAATTTAAAAATGCTTTCTTAATATTAATTTATTAATTAATTAATTAATTAATTAAT 300
Qy 1772 TGCAAAAATCATCATCAACATATCCAACTTGAAATCTCTATGTCACAGAGTAGAA 1831
Db 301 TGCAAAAATCATCATCAACATATCCAACTTGAAATCTCTATGTCACAGAGTAGAA 360
Qy 1832 AATAAATTTTACTAGATCAAAATCTCTAATCATCATTAATTAATGTTTACAAAATCTAAT 1891
Db 361 AATAAATTTTACTAGATCAAAATCTCTAATCATCATTAATTAATGTTTACAAAATCTAAT 420
Qy 1892 TAAACCCACCTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1951
Db 421 TAAACCCACCTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480
Qy 1952 CAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2011
Db 481 CAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Qy 2012 TCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2071
Db 541 TCAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Qy 2072 TGTGAACATTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2131
Db 601 TGTGAACATTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 660
Qy 2132 TGTGAACATTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2180
Db 661 TGTGAACATTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 709

RESULT 7
US-09-545-244A-11
; Sequence 11, Application US/09545244A
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? : SEQUENCE CHARACTERISTICS:
? : LENGTH: 1863 base pairs
? : TYPE: nucleic acid
? : STRANDEDNESS: single
? : TOPOLOGY: linear
? : MOLECULE TYPE: cDNA
? : HYPOTHETICAL: NO
? :
US-08-525-507-16

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Query Match	8.1%	Score 257.2;	DB 1;	Length 1863;
Best Local Similarity	98.9%;	Pred. No. 5.6e-47;		
Matches 259; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	2992	TCGCATCGTTCAAAACATTTGGCAATTAAGTTTCTTAAGATGAATCCGTTGCCGCTTT	2981
QY <td>1662</td> <td>CCCGATCGTTCAAAACATTTGGCAATTAAGTTTCTTAAGATGAATCCGTTGCCGCTTT</td> <td>1661</td>	1662	CCCGATCGTTCAAAACATTTGGCAATTAAGTTTCTTAAGATGAATCCGTTGCCGCTTT	1661
Db <td>2982</td> <td>GGCATGATTAATCAATTAATTTCTGTGAATTCGTTAAGCATGTATATTAATCAATGTAA</td> <td>3041</td>	2982	GGCATGATTAATCAATTAATTTCTGTGAATTCGTTAAGCATGTATATTAATCAATGTAA	3041
QY <td>1662</td> <td>GGCATGATTAATCAATTAATTTCTGTGAATTAACGTTAAGCATGTATATTAATCAATGTAA</td> <td>1722</td>	1662	GGCATGATTAATCAATTAATTTCTGTGAATTAACGTTAAGCATGTATATTAATCAATGTAA	1722
Db <td>3042</td> <td>TGCATGACGCTTAATTATGATGAGTGCGTTTATTATGATTAAAGTCCGCCAATTATACATTTAA</td> <td>3101</td>	3042	TGCATGACGCTTAATTATGATGAGTGCGTTTATTATGATTAAAGTCCGCCAATTATACATTTAA	3101
QY <td>1722</td> <td>TGCATGACGCTTAATTATGATGAGTGCGTTTATTATGATTAAAGTCCGCCAATTATACATTTAA</td> <td>1781</td>	1722	TGCATGACGCTTAATTATGATGAGTGCGTTTATTATGATTAAAGTCCGCCAATTATACATTTAA	1781
Db <td>3102</td> <td>TACGCGATGAGAAAACAAAATATGCGCGCGCAAACTGGGATTAATTATCGCGCGCGGTGTCA</td> <td>3161</td>	3102	TACGCGATGAGAAAACAAAATATGCGCGCGCAAACTGGGATTAATTATCGCGCGCGGTGTCA	3161
QY <td>1782</td> <td>TACGCGATGAGAAAACAAAATATGCGCGCGCAAACTGGGATTAATTATCGCGCGCGGTGTCA</td> <td>1841</td>	1782	TACGCGATGAGAAAACAAAATATGCGCGCGCAAACTGGGATTAATTATCGCGCGCGGTGTCA	1841
Db <td>3162</td> <td>TCTATGTTACTGATCGGAATTC</td> <td>3183</td>	3162	TCTATGTTACTGATCGGAATTC	3183
QY <td>1842</td> <td>TCTATGTTACTGATCGGAATTC</td> <td>1863</td>	1842	TCTATGTTACTGATCGGAATTC	1863

RESULT 11
 US-08-475-427-9
 / Sequence 9, Application US/08475427
 / Patent No. 5859340
 / GENERAL INFORMATION:
 / APPLICANT: DUBOIS, Michel
 / APPLICANT: GRISON, Rene
 / APPLICANT: LEGUAY, Jean-Jacques
 / APPLICANT: PIGNARD, Annie
 / APPLICANT: TOPPAN, Alain
 / TITLE OF INVENTION: Recombinant gene coding for a protein
 / TITLE OF INVENTION: having endochitinase activity or for a precursor thereof
 / NUMBER OF SEQUENCES: 15
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Foley & Lardner
 / STREET: 3000 K Street, N.W., Suite 500
 / CITY: Washington, D.C.
 / COUNTRY: USA
 / ZIP: 20007-5109
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/475,427
 / FILING DATE: 07-JUN-1995
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/842,165
 / FILING DATE: 01-MAY-1992
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: WO PCT/FR91/00607
 / FILING DATE: 21-JUL-1991
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: FR 90 09460
 / FILING DATE: 24-JUL-1990
 / ATTORNEY/AGENT INFORMATION:
 / NAME: BERT, Stephen A.
 / REGISTRATION NUMBER: 29,768

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1 REFERENCE/DOCKET NUMBER: 16781/564/BEID
2
3 TELECOMMUNICATION INFORMATION:
4
5 TELEPHONE: (202)672-5300
6
7 TELEFAX: (202)672-5399
8
9 TELEX: 904136
10
11 INFORMATION FOR SEQ ID NO: 9:
12
13 SEQUENCE CHARACTERISTICS:
14
15 LENGTH: 1663 base pairs
16
17 TYPE: nucleic acid
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19 STRANDEDNESS: single
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21 TOPOLOGY: linear
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23 MOLECULE TYPE: cDNA
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25 HYPOTHEITICAL: NO
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Best Local Similarity	98.9%	Pred. No.	5.6e-47				
Matches	259	Conservative	0	Mismatches	3	Indels	0
						Gaps	0

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1602	CCGATCGTTCACACATTTGGCAATAAAGTTCTTAAGATTGATCCGTGGCGGCTT
QY	Db
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3042	TGCATGACGTTATTTATGAGATGGGTTTTATATGATTAGATCCGCGCAATTATACATTAA
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1782	TACCGGATAGAAAACAAAATATGCGCGCGCAAACTGGGATAATTATGCGCGCGGCTGCA
QY	Db
3162	TCTATGTTACTAGATCGAATTC 3183
1842	TCTATGTTACTAGATCGAATTC 1863

RESULT 12
 US-07-842-165-9
 ; Sequence 9, Application us/07842165
 ; Patent No. 5932698
 ;
 ; GENERAL INFORMATION:
 APPLICANT: DUBOIS, Michel
 APPLICANT: GRISON, Rene
 APPLICANT: LEGUAY, Jean-Jacques
 APPLICANT: PIGNARD, Annie
 APPLICANT: TOPPAN, Alain
 TITLE OF INVENTION: Recombinant gene coding for a protein
 TITLE OF INVENTION: having endochitinase activity or for a precursor thereof
 NUMBER OF SEQUENCES: 15
 ;
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: FOLEY & LARDNER
 STREET: King Street Station, Suite 500, 1800 Diagonal
 STREET: Road, PO Box 299
 CITY: ALEXANDRIA
 STATE: VIRGINIA
 COUNTRY: USA
 ZIP: 22313-0299
 ;
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/842,165
 FILING DATE: 19920501
 CLASSIFICATION: 435
 ;
 ATTORNEY/AGENT INFORMATION:
 NAME: SAKÉ, Bernhard D
 REGISTRATION NUMBER: 28,665
 ;

REFERENCE/DOCKET NUMBER: 16781/348
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1863 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-07-842-165-9

Query Match 8.1%; Score 257.2; DB 2; Length 1863;
Best Local Similarity 98.9%; Pred. No. 5.6e-47;
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1842 TCTATGTTACTAGATCGAATTC 1863

RESULT 13
US-08-525-507-14
Sequence 14, Application US/08525507
Patent No. 5792932
GENERAL INFORMATION:
APPLICANT: MARCO, Yves
APPLICANT: ROBY, Dominique
APPLICANT: SCHNEIDER, Michel
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Plant promoter, microorganisms and plant
TITLE OF INVENTION: cells containing a unit for the expression of a protein of
TITLE OF INVENTION: interest comprising said promoter.
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DENNISON, MERELOLE, POLLACK & SCHEINER
STREET: 612 Crystal Square 4 - 1745 Jefferson Davis
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 666
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,507
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 03299
FILING DATE: 23-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO FR94/00316
FILING DATE: 23-MAR-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 412-1155
TELEFAX: (703) 412-1161
TELEX: 82-4412 TOWMBAT
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4284 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
US-08-525-507-14

Query Match 8.1%; Score 257.2; DB 1; Length 4284;
Best Local Similarity 98.9%; Pred. No. 7.1e-47;
Matches 259; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 4263 TCTATGTTACTAGATCGAATTC 4284

RESULT 14
US-08-673-768-1
Sequence 1, Application US/08673768
Patent No. 5952546
GENERAL INFORMATION:
APPLICANT: Bedbrook, John R.
APPLICANT: Dunsmuir, Pamela
APPLICANT: Howie, William J.
APPLICANT: Joe, Lawrence K.
APPLICANT: Lee, Kathleen Y.
TITLE OF INVENTION: Delayed Ripening Tomato Plants
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,768
FILING DATE: 27-JUN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,721
FILING DATE: 30-JUN-1995

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OM nucleic - nucleic search, using sw model

Run on: June 10, 2004, 05:04:35 ; Search time 5033 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 18: /cgn2_6/ptodata/2/pubdna/US60_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubdna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	730.2	22.9	2595	16	US-10-369-493-38940
5	730.2	22.9	2595	17	US-10-369-493-38964
6	730.2	22.9	2595	16	US-10-369-493-38966
7	730.2	22.9	9323	17	US-10-607-538-4
8	730.2	22.9	9323	17	US-10-607-538-4
9	712.2	22.4	747	15	US-10-187-339-5
10	711.8	22.4	720	16	US-10-369-493-38936
11	711.8	22.4	720	16	US-10-369-493-38940
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13	711.8	22.4	720	16	US-10-369-493-38966
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27	433.4	13.6	2544	15	US-10-187-339-9	Sequence 9, Appl1
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29	428.0	8.2	4280	15	US-10-027-880-4	Sequence 4, Appl1
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31	255.6	8.0	17458	15	US-10-055-001A-25	Sequence 24, Appl1
32	255.6	8.0	17476	15	US-10-055-001A-24	Sequence 7, Appl1
33	255.6	8.0	17476	15	US-10-385-546-7	Sequence 26, Appl1
34	255.6	8.0	17681	15	US-10-055-001A-26	Sequence 23, Appl1
35	255.6	8.0	17862	15	US-10-055-001A-23	Sequence 13, Appl1
36	255.6	8.0	18691	15	US-10-055-001A-13	Sequence 14, Appl1
37	255.2	8.0	8074	14	US-10-047-542-14	Sequence 4, Appl1
38	255	8.0	6548	9	US-09-509-945-4	Sequence 12, Appl1
39	254.2	8.0	2709	15	US-10-260-960-12	Sequence 12, Appl1
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41	254.2	8.0	5281	9	US-09-921-263-2	Sequence 2, Appl1
42	254.2	8.0	5909	15	US-10-191-381-16	Sequence 16, Appl1
43	253.8	8.0	1908	15	US-10-260-960-3	Sequence 3, Appl1
44	253	7.9	2115	15	US-10-260-960-3	Sequence 3, Appl1
45	253	7.9	2115	15	US-10-260-562-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-10-072-077A-1
Sequence 1, Application US/10072077A
; Publication No. US2003015009A1
; GENERAL INFORMATION:
; APPLICANT: Gallie, Daniel R.
; APPLICANT: Young, Todd E.
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-121500US
; CURRENT APPLICATION NUMBER: US/10/072.077A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3183
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: Promoter
; LOCATION: (1)..(3183)
; OTHER INFORMATION: sense-sense-associated gene 12-1 (SAG12-1) promoter
US-10-072-077A-1

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QY	61	CTCGGACACCGAGTCGTTTATTTAGAAACCCGATTTTATTTAGACTGAGAC	120
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2161 CATTTAATCTTTCTTAATAAATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 2220
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2221 AAGAGCAAGCAAGCAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 2280
2221 AAGAGCAAGCAAGCAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 2280
2281 CCGGTCATGATGTTGCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2340
2281 CCGGTCATGATGTTGCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2340

QY 2341 AAAGAAAGAGCGCTCTTACTTGAATGATGGGCTCTGGTGAAGGATATATGCAACC 2400
Db 2341 AAAAGAAAGAGCGCTCTTACTTGAATGATGGGCTCTGGTGAAGGATATATGCAACC 2400
QY 2401 AAGGAGCTCATAGAGCTGATGAGAGGATGATATATGATGAGGCAAGGCGGCTT 2460
Db 2401 AAGGAGCTCATAGAGCTGATGAGAGGATGATATATGATGAGGCAAGGCGGCTT 2460
QY 2461 ATTCTTGAAGGAGATCCACCTCGTGTCTCACTGATGAGGCAAGGATATGAGT 2520
Db 2461 ATTCTTGAAGGAGATCCACCTCGTGTCTCACTGATGAGGCAAGGATATGAGT 2520
QY 2521 GCAAGATTTTCTTGGCATATATATGCGCAAGTTACCCGACCAAGAGACCTTATGAA 2580
Db 2521 GCAAGATTTTCTTGGCATATATATGCGCAAGTTACCCGACCAAGAGACCTTATGAA 2580
QY 2581 GCGGCGAAGGCGAGGATTAAGCAGATGTTGCAACCCGCTGAGGCAATTCATATTCAA 2640
Db 2581 GCGGCGAAGGCGAGGATTAAGCAGATGTTGCAACCCGCTGAGGCAATTCATATTCAA 2640
QY 2641 GAGTTGGTTTATCTTGGATGAACCTGCGTGAAGCCCATTTGAAAGAGATGATGA 2700
Db 2641 GAGTTGGTTTATCTTGGATGAACCTGCGTGAAGCCCATTTGAAAGAGATGATGA 2700
QY 2701 TATGATATGCGCATGTTGTTGCTAGCCAGAACGATCAAGGATATCTTATGAG 2760
Db 2701 TATGATATGCGCATGTTGTTGCTAGCCAGAACGATCAAGGATATCTTATGAG 2760
QY 2761 CTTCAGCAAAATATGAGAGTATGATGATTAATGGGATCGCTGAGGATATTCATCAT 2820
Db 2761 CTTCAGCAAAATATGAGAGTATGATGATTAATGGGATCGCTGAGGATATTCATCAT 2820
QY 2821 GCGGCGCAACAGAAAGAAATTCGCCAAGTTAAAGGAGCGGCTTTCAGAGATTCGAA 2880
Db 2821 GCGGCGCAACAGAAAGAAATTCGCCAAGTTAAAGGAGCGGCTTTCAGAGATTCGAA 2880
QY 2881 GGTCAATCCGTTGCGAATATATGATGATGATGATGATGATGATGATGATGATGAT 2940
Db 2881 GGTCAATCCGTTGCGAATATATGATGATGATGATGATGATGATGATGATGATGAT 2940
QY 2941 GCGAATTAAGTTCTTAAGATTTGAATCTGTTGCGGCTTTCAGATGATTAATGAT 3000
Db 2941 GCGAATTAAGTTCTTAAGATTTGAATCTGTTGCGGCTTTCAGATGATTAATGAT 3000
QY 3001 TTCTGTGAATTAAGTATGATGATGATTAATTAATTAATGATGATGATGATGATGAT 3060
Db 3001 TTCTGTGAATTAAGTATGATGATTAATTAATTAATTAATGATGATGATGATGATGAT 3060
QY 3061 GATGGGTTTATGATTAAGTATGATGATGATGATGATGATGATGATGATGATGAT 3120
Db 3061 GATGGGTTTATGATTAAGTATGATGATGATGATGATGATGATGATGATGATGAT 3120
QY 3121 TATGGCGGCAACGAGTAAATTAATGCGGCGGCTGATGATGATGATGATGATGAT 3180
Db 3121 TATGGCGGCAACGAGTAAATTAATGCGGCGGCTGATGATGATGATGATGATGAT 3180
QY 3181 TTC 3183
Db 3181 TTC 3183

RESULT 2
US-10-363-723-2
; Sequence 2, Application US/10363723
; Publication No. US20040025205A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture Victoria Services Pty Ltd
; APPLICANT: La Trobe University
; APPLICANT: SPANGENBERG, German
; APPLICANT: LIN, Yi Han
; APPLICANT: PARISH, Roger W.
; APPLICANT: LI, Song Feng W.

APPLICANT: HEAZLEWOOD, Joshua W.
; TITLE OF INVENTION: Manipulation of plant senescence
; FILE REFERENCE: 14403US
; CURRENT APPLICATION NUMBER: US/10/363,723
; PRIOR FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: AU P09946
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: PCT/AU01/01092
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1988
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-363-723-2

Query March 23.0%; Score 733.4; DB 17; Length 1988;
Best Local Similarity 96.0%; Pred. No. 3.1e-125;
Matches 752; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 2139 TAATCAATTAAGAGCAAAAGTCAATTAATCTTCTTAAACATGAGACCTGATCTAAT 2198
Db 647 TAATATAAATCAAGTTGATTAATCAATTAATCAATTAATCAATTAATCAATTAAT 706
QY 2199 TTTTGATCCAACTTGACAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2258
Db 707 TTTTGATCCAACTTGACAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 766
QY 2259 GCTTCAGATCTTCTGCTGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2318
Db 767 GCTTCAGATCTTCTGCTGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 826
QY 2319 ACGACCAACAGTGAAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2378
Db 827 ACGACCAACAGTGAAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 886
QY 2379 GGTGAGGATATCATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2438
Db 887 GGTGAGGATATCATGCGAG 946
QY 2439 TCATGAGGCAACGAGGAGGAGGATTTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2498
Db 947 TCATGAGGCAACGAGGAGGAGGATTTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1006
QY 2499 GAGCGGAAGAGATTAAG 2558
Db 1007 GAGCGGAAGAGATTAAG 1066
QY 2559 CGACCAAGAGAGATTAAG 2618
Db 1067 CGACCAAGAGAGATTAAG 1126
QY 2619 TGCAGGCAATCTATTAATTAAG 2678
Db 1127 TGCAGGCAATCTATTAATTAAG 1186
QY 2679 CATCTGAAGAGAGATTAAG 2738
Db 1187 CATCTGAAGAGAGATTAAG 1246
QY 2739 CAGGCGAGATTAAG 2798
Db 1247 CAGGCGAGATTAAG 1306
QY 2799 GAGTCAAGAGATTAAG 2858
Db 1307 GAGTCAAGAGATTAAG 1366
QY 2859 AGCGGCTTTCAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2918
Db 1367 AGCGGCTTTCAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1426

QY 2919 GAG 2921
Db 1427 GCG 1429

RESULT 3

US-10-369-324-3
; Sequence 3, Application US/10369324
; Publication No. US2003022131A1
; GENERAL INFORMATION:
; APPLICANT: ROMMENS, CAIUS
; APPLICANT: YE, JINGSONG
; APPLICANT: MENENDEZ-HUMARA, JAIME
; APPLICANT: YAN, HUA
; APPLICANT: RICHARD, CRAIG
; APPLICANT: BRINKHOFF, W. LEIGH
; APPLICANT: SWORDS, KATHY M. M.
; TITLE OF INVENTION: PRECISE BREEDING
; FILE REFERENCE: 058951/0162
; CURRENT APPLICATION NUMBER: US/10/369,324
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/357,661
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 60/377,602
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Expression
US-10-369-324-3

Query Match 22.9%; Score 730.2; DB 16; Length 2595;
Best Local Similarity 99.6%; Pred. No. 1.4e-124;
Matches 732; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2187 CCTGATCTAATTTTCGGTCCAACTTGCACAGAAAGACGACCGGATAGCTCTTGC 2246
Db 1166 CCGATCTAATTTTCGGTCCAACTTGCACAGAAAGACGACCGGATAGCTCTTGC 1225
QY 2247 CCAGAGACAGGCGCTTCCAGTCTTCCGCTTGTGATGCGGTCAATGTCCTCAACTATC 2306
Db 1226 CCAGAGACAGGCGCTTCCAGTCTTCCGCTTGTGATGCGGTCAATGTCCTCAACTATC 1285
QY 2307 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAGAGAGACGCGCTCTTCACTTGA 2366
Db 1286 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAGAGAGACGCGCTCTTCACTTGA 1345
QY 2367 TGATGGGCTCTGGTGGAGGGTATATGCGACCAAGCAAGCTCATAGGCTGATGCA 2426
Db 1346 TGATGGGCTCTGGTGGAGGGTATATGCGACCAAGCAAGCTCATAGGCTGATGCA 1405
QY 2427 GGAGGTGATTAATCATGAGGCCAACGCGCGGCTTATCTTGAAGGAGATCCACTCGTT 2486
Db 1406 GGAGGTGATTAATCATGAGGCCAACGCGCGGCTTATCTTGAAGGAGATCCACTCGTT 1465
QY 2487 GCTCAACTGATGCGGCAAAACAGCTATTGAGTGAAGATTTTCGTTGGCAATATTTCG 2546
Db 1466 GCTCAACTGATGCGGCAAAACAGCTATTGAGTGAAGATTTTCGTTGGCAATATTTCG 1525
QY 2547 CCAGAGTAAACCGACCAAGAGACCTTCAAGAAAGCGGCAAGGCGCAGAGTTAAGAGAT 2606
Db 1526 CCAGAGTAAACCGACCAAGAGACCTTCAAGAAAGCGGCAAGGCGCAGAGTTAAGAGAT 1585
QY 2607 GTTGACCCCGCTGACGAGCCATTCTATTATCAAGAGTTGTTTATCTTTGAATGAAACC 2666
Db 1586 GTTGACCCCGCTGACGAGCCATTCTATTATCAAGAGTTGTTTATCTTTGAATGAAACC 1645
QY 2667 TCGGCTGAGGCGCATTTCTGAAGAGATGATGATGATGATGATGATGATGATGATGATG 2726

Db 1646 TCGGCTGAGGCGCATTTCTGAAGAGATGATGATGATGATGATGATGATGATGATGATG 1705
QY 2727 CCAGAACAGATCAGGACAGATATGCTATTGACGAGTGAAGAAATGGAAGTAAAGTT 2786
Db 1706 CCAGAACAGATCAGGACAGATATGCTATTGACGAGTGAAGAAATGGAAGTAAAGTT 1765
QY 2787 GATTATGAGATGCTCAGGAGATTTTCAATCCATGCGCGCCCAACAGAAATATCC 2846
Db 1766 GATTATGAGATGCTCAGGAGATTTTCAATCCATGCGCGCCCAACAGAAATATCC 1825
QY 2847 CCAGTTAAGCAGCGGCTTTCAGAGGATTCGAAGTCAATCCGTTGGAATGATTAAGT 2906
Db 1826 CCAGTTAAGCAGCGGCTTTCAGAGGATTCGAAGTCAATCCGTTGGAATGATTAAGT 1885
QY 2907 TACGCCAGCCCTGAG 2921
Db 1886 TACGCCAGCCCTGCG 1900

RESULT 4

US-10-392-301-3
; Sequence 3, Application US/10392301
; Publication No. US2004000343A1
; GENERAL INFORMATION:
; APPLICANT: WEEKS, J. TROY
; APPLICANT: ROMMENS, CAIUS
; TITLE OF INVENTION: REFINED PLANT TRANSFORMATION
; FILE REFERENCE: 058951/0164
; CURRENT APPLICATION NUMBER: US/10/392,301
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/365,527
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/377,597
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Cytokinin IPT
US-10-392-301-3

Query Match 22.9%; Score 730.2; DB 16; Length 2595;
Best Local Similarity 99.6%; Pred. No. 1.4e-124;
Matches 732; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2187 CCTGATCTAATTTTCGGTCCAACTTGCACAGAAAGACGACCGGATAGCTCTTGC 2246
Db 1166 CCGATCTAATTTTCGGTCCAACTTGCACAGAAAGACGACCGGATAGCTCTTGC 1225
QY 2247 CCAGAGACAGGCGCTTCCAGTCTTCCGCTTGTGATGCGGTCAATGTCCTCAACTATC 2306
Db 1226 CCAGAGACAGGCGCTTCCAGTCTTCCGCTTGTGATGCGGTCAATGTCCTCAACTATC 1285
QY 2307 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAGAGAGACGCGCTCTTCACTTGA 2366
Db 1286 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAGAGAGACGCGCTCTTCACTTGA 1345
QY 2367 TGATGGGCTCTGGTGGAGGGTATATGCGACCAAGCAAGCTCATAGGCTGATGCA 2426
Db 1346 TGATGGGCTCTGGTGGAGGGTATATGCGACCAAGCAAGCTCATAGGCTGATGCA 1405
QY 2427 GGAGGTGATTAATCATGAGGCCAACGCGGCTTATCTTGAAGGAGATCCACTCGTT 2486
Db 1406 GGAGGTGATTAATCATGAGGCCAACGCGGCTTATCTTGAAGGAGATCCACTCGTT 1465
QY 2487 GCTCAACTGATGCGGCAAAACAGCTATTGAGTGAAGATTTTCGTTGGCAATATTTCG 2546
Db 1466 GCTCAACTGATGCGGCAAAACAGCTATTGAGTGAAGATTTTCGTTGGCAATATTTCG 1525

OTHER INFORMATION: nucleotide sequence
US-10-369-324-4

Query Match 22.9%; Score 730.2; DB 16; Length 9323;
Best Local Similarity 99.6%; Pred. No. 2.5e-124;
Matches 732; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2187 CCGCATCTAATTTTGGTCCAACTTGCACAGAAAACGACGACCGGATAGCTCTGC 2246
DB 7646 CCGCATCTAATTTTGGTCCAACTTGCACAGAAAACGACGACCGGATAGCTCTGC 7705
QY 2247 CCAGCAGACAGAGGCTTCCAGTCTTTCGCTTGCATCGGCTCAATCGTCTCAACTATC 2306
DB 7706 CCAGCAGACAGAGGCTTCCAGTCTTTCGCTTGCATCGGCTCAATCGTCTCAACTATC 7765
QY 2307 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAAGAAAGACGCGCTCTCACTTGA 2366
DB 7766 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAAGAAAGACGCGCTCTCACTTGA 7825
QY 2367 TGATCGGCTCTGTGTGAGGGTATCATCGACGACCAAGCTATCATAGGCTGATCGA 2426
DB 7826 TGATCGGCTCTGTGTGAGGGTATCATCGACGACCAAGCTATCATAGGCTGATCGA 7885
QY 2427 GGAGGTGATATATCATGAGGCGCAAGCGGCTTATCTTGAGGGAGATCCACTGCT 2486
DB 7886 GGAGGTGATATATCATGAGGCGCAAGCGGCTTATCTTGAGGGAGATCCACTGCT 7945
QY 2487 GCTCACTGATGCGCGGAAACAGCTATGAGTGCAGATTTTGGTGGCAATTTATTCG 2546
DB 7946 GCTCACTGATGCGCGGAAACAGCTATGAGTGCAGATTTTGGTGGCAATTTATTCG 8005
QY 2547 CCAGAACTTACCCGACCAAGAGACCTTCAATGAAGCGGCAAGGCGCAGAGTTAAGCAT 2606
DB 8006 CCAGAACTTACCCGACCAAGAGACCTTCAATGAAGCGGCAAGGCGCAGAGTTAAGCAT 8065
QY 2607 GTTGCACCCCGCTGAGGCTCATTTATTCAGAGTGGTATCTTTGAGAGTGAAC 2666
DB 8066 GTTGCACCCCGCTGAGGCTCATTTATTCAGAGTGGTATCTTTGAGAGTGAAC 8125
QY 2667 TCGGCTGAGGCGCATTTCTGAAAGAGATGATGATGATGATGATGATGATGATGATG 2726
DB 8126 TCGGCTGAGGCGCATTTCTGAAAGAGATGATGATGATGATGATGATGATGATGATG 8185
QY 2727 CCAGAACTTACCCGACCAAGAGACCTTCAATGAAGCGGCAAGGCGCAGAGTTAAGCAT 2786
DB 8186 CCAGAACTTACCCGACCAAGAGACCTTCAATGAAGCGGCAAGGCGCAGAGTTAAGCAT 8245
QY 2787 GATTAATGGAGTCCGCTCAGAGATATTCATTCATTCATTCATTCATTCATTCATTCATTC 2846
DB 8246 GATTAATGGAGTCCGCTCAGAGATATTCATTCATTCATTCATTCATTCATTCATTCATTC 8305
QY 2847 CCAGAACTTACCCGACCAAGAGACCTTCAATGAAGCGGCAAGGCGCAGAGTTAAGCAT 2906
DB 8306 CCAGAACTTACCCGACCAAGAGACCTTCAATGAAGCGGCAAGGCGCAGAGTTAAGCAT 8365
QY 2907 TACGCCAGCCCTGAG 2921
DB 8366 TACGCCAGCCCTGCG 8380
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RESULT 7
US-10-607-538-4

Sequence 4, Application US/10607538
Publication No. US20040107455A1
GENERAL INFORMATION:
APPLICANT: ROMMENS, CAIUS
APPLICANT: YE, JINGSONG
APPLICANT: HIMARA, JAIME M.
APPLICANT: YAN, HUA
APPLICANT: SMODS, KATHY
TITLE OF INVENTION: PRECISE BREEDING
FILE REFERENCE: 058951/0167
CURRENT APPLICATION NUMBER: US/10/607,538

CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 10/369,324
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/357,661
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 60/377,602
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 4
LENGTH: 9323
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: pSIM111
US-10-607-538-4

Query Match 22.9%; Score 730.2; DB 17; Length 9323;
Best Local Similarity 99.6%; Pred. No. 2.5e-124;
Matches 732; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2187 CCGCATCTAATTTTGGTCCAACTTGCACAGAAAACGACGACCGGATAGCTCTGC 2246
DB 7646 CCGCATCTAATTTTGGTCCAACTTGCACAGAAAACGACGACCGGATAGCTCTGC 7705
QY 2247 CCAGCAGACAGAGGCTTCCAGTCTTTCGCTTGCATCGGCTCAATCGTCTCAACTATC 2306
DB 7706 CCAGCAGACAGAGGCTTCCAGTCTTTCGCTTGCATCGGCTCAATCGTCTCAACTATC 7765
QY 2307 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAAGAAAGACGCGCTCTCACTTGA 2366
DB 7766 AACCGAAGCGGACGACCAACAGTGAAGAACTGAAAGAAAGACGCGCTCTCACTTGA 7825
QY 2367 TGATCGGCTCTGTGTGAGGGTATCATCGACGACCAAGCTATCATAGGCTGATCGA 2426
DB 7826 TGATCGGCTCTGTGTGAGGGTATCATCGACGACCAAGCTATCATAGGCTGATCGA 7885
QY 2427 GGAGGTGATATATCATGAGGCGCAAGCGGCTTATCTTGAGGGAGATCCACTGCT 2486
DB 7886 GGAGGTGATATATCATGAGGCGCAAGCGGCTTATCTTGAGGGAGATCCACTGCT 7945
QY 2487 GCTCACTGATGCGCGGAAACAGCTATGAGTGCAGATTTTGGTGGCAATTTATTCG 2546
DB 7946 GCTCACTGATGCGCGGAAACAGCTATGAGTGCAGATTTTGGTGGCAATTTATTCG 8005
QY 2547 CCAGAACTTACCCGACCAAGAGACCTTCAATGAAGCGGCAAGGCGCAGAGTTAAGCAT 2606
DB 8006 CCAGAACTTACCCGACCAAGAGACCTTCAATGAAGCGGCAAGGCGCAGAGTTAAGCAT 8065
QY 2607 GTTGCACCCCGCTGAGGCTCATTTATTCAGAGTGGTATCTTTGAGAGTGAAC 2666
DB 8066 GTTGCACCCCGCTGAGGCTCATTTATTCAGAGTGGTATCTTTGAGAGTGAAC 8125
QY 2667 TCGGCTGAGGCGCATTTCTGAAAGAGATGATGATGATGATGATGATGATGATGATG 2726
DB 8126 TCGGCTGAGGCGCATTTCTGAAAGAGATGATGATGATGATGATGATGATGATGATG 8185
QY 2727 CCAGAACTTACCCGACCAAGAGACCTTCAATGAAGCGGCAAGGCGCAGAGTTAAGCAT 2786
DB 8186 CCAGAACTTACCCGACCAAGAGACCTTCAATGAAGCGGCAAGGCGCAGAGTTAAGCAT 8245
QY 2787 GATTAATGGAGTCCGCTCAGAGATATTCATTCATTCATTCATTCATTCATTCATTCATTC 2846
DB 8246 GATTAATGGAGTCCGCTCAGAGATATTCATTCATTCATTCATTCATTCATTCATTCATTC 8305
QY 2847 CCAGAACTTACCCGACCAAGAGACCTTCAATGAAGCGGCAAGGCGCAGAGTTAAGCAT 2906
DB 8306 CCAGAACTTACCCGACCAAGAGACCTTCAATGAAGCGGCAAGGCGCAGAGTTAAGCAT 8365
QY 2907 TACGCCAGCCCTGAG 2921
DB 8366 TACGCCAGCCCTGCG 8380
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RESULT 8
US-10-187-339-12
; Sequence 12, Application US/10187339
; Publication No. US20030084478A1
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.,
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
; TITLE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/10/187,339
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/434,837
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,185
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-187-339-12

Query Match 22.5%; Score 714.8; DB 15; Length 723;
Best Local Similarity 99.7%; Pred. No. 5.2e-122;
Matches 716; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2187 CCTGCATTAATTTTGGTCCAACTTGACAGAGAAAGCAGACCGGATAGCTTGGC 2246
DB 6 CCTGCATTAATTTTGGTCCAACTTGACAGAGAAAGCAGACCGGATAGCTTGGC 65
QY 2247 CCAGCAGACAGAGGCTTCCAGTCTTTCGCTTATCGAGGCTCCATCGTCTCACTATC 2306
DB 66 CCAGCAGACAGAGGCTTCCAGTCTTTCGCTTATCGAGGCTCCATCGTCTCACTATC 125
QY 2307 AACCGGAAAGCGGAGCAGCAAGATGGAAGAACTGAAAGGAAAGCGCTCTTACCTTGA 2366
DB 126 AACCGGAAAGCGGAGCAGCAAGATGGAAGAACTGAAAGGAAAGCGCTCTTACCTTGA 185
QY 2367 TGATCGGCTCTGGTGGAGGGATTCATGAGCCAGCAAGCACTCATCTAGGCTGATGA 2426
DB 186 TGATCGGCTCTGGTGGAGGGATTCATGAGCCAGCAAGCACTCATCTAGGCTGATGA 245
QY 2427 GAGGCTGATATCATGAGGCGCAAGCGGCGCTTATCTTGAGGAGGATCCACTGCTT 2486
DB 246 GAGGCTGATATCATGAGGCGCAAGCGGCGCTTATCTTGAGGAGGATCCACTGCTT 305
QY 2487 GCTCACTGCAATGGCGCGAAGCAGCTATTGAGTGCAGATTTTGGTGGCATATTATTCG 2546
DB 306 GCTCACTGCAATGGCGCGAAGCAGCTATTGAGTGCAGATTTTGGTGGCATATTATTCG 365
QY 2547 CCACAGTACCCGACCAAGAGACCTTCATGAAGCGGCGCAAGCGCAAGTAAAGCAT 2606
DB 366 CCACAGTACCCGACCAAGAGACCTTCATGAAGCGGCGCAAGCGCAAGTAAAGCAT 425
QY 2607 GTTGCAACCCCGCTGAGGCGCATTTCTATTATTCAGAGTTGTTTATCTTTGGAATGAAC 2666
DB 426 GTTGCAACCCCGCTGAGGCGCATTTCTATTATTCAGAGTTGTTTATCTTTGGAATGAAC 485
QY 2667 TGGGCTGAGGCGCATTTCTGAAGAGATGATGATATGATATGCAATGTTGTTGCTAG 2726
DB 486 TGGGCTGAGGCGCATTTCTGAAGAGATGATGATATGATATGCAATGTTGTTGCTAG 545
QY 2727 CCAGAACCCAGTACCGGAGATATGCTATTCAGCTTGAAGCAATATGAAAGGTAAGTT 2786
DB 546 CCAGAACCCAGTACCGGAGATATGCTATTCAGCTTGAAGCAATATGAAAGGTAAGTT 605
QY 2787 GATTAAATGGATCGCTCAGAGATATTTTCATCATGCGGCCAAGAGAAAGAAATTCCTC 2846
DB 606 GATTAAATGGATCGCTCAGAGATATTTTCATCATGCGGCCAAGAGAAAGAAATTCCTC 665
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RESULT 9
US-10-187-339-5
; Sequence 5, Application US/10187339
; Publication No. US20030084478A1
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.,
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
; TITLE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/10/187,339
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/434,837
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,185
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-187-339-5

Query Match 22.4%; Score 712.2; DB 15; Length 747;
Best Local Similarity 99.6%; Pred. No. 1.6e-121;
Matches 714; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2188 CTGCATTAATTTTGGTCCAACTTGACAGAGAAAGCAGACCGGATAGCTTGGC 2247
DB 18 CTGCATTAATTTTGGTCCAACTTGACAGAGAAAGCAGACCGGATAGCTTGGC 77
QY 2248 CAGCAGACAGGCTTCCAGTCTTTCGCTTATCGAGGCTCCATCGTCTCACTATCA 2307
DB 78 CAGCAGACAGGCTTCCAGTCTTTCGCTTATCGAGGCTCCATCGTCTCACTATCA 137
QY 2308 ACCGGAAGCGGAGCAGCAAGATGGAAGAACTGAAAGGAAAGCGCTCTTACCTTGA 2367
DB 138 ACCGGAAGCGGAGCAGCAAGATGGAAGAACTGAAAGGAAAGCGCTCTTACCTTGA 197
QY 2368 GATGGGCTCTGGTGGAGGGATTCATGAGCCAGCAAGCACTCATCTAGGCTGATGA 2427
DB 198 GATGGGCTCTGGTGGAGGGATTCATGAGCCAGCAAGCACTCATCTAGGCTGATGA 257
QY 2428 GAGGCTGATATCATGAGGCGCAAGCGGCGCTTATCTTGAGGAGGATCCACTGCTT 2487
DB 258 GAGGCTGATATCATGAGGCGCAAGCGGCGCTTATCTTGAGGAGGATCCACTGCTT 317
QY 2488 CTCACTGCAATGGCGCGAAGCAGCTATTGAGTGCAGATTTTGGTGGCATATTATTCG 2547
DB 318 CTCACTGCAATGGCGCGAAGCAGCTATTGAGTGCAGATTTTGGTGGCATATTATTCG 377
QY 2548 CACAAATTACCCGACCAAGAGACCTTCATGAAGCGGCGCAAGCGCAAGTAAAGCAT 2607
DB 378 CACAAATTACCCGACCAAGAGACCTTCATGAAGCGGCGCAAGCGCAAGTAAAGCAT 437
QY 2608 TTGCAACCCCGCTGAGGCGCATTTCTATTATTCAGAGTTGTTTATCTTTGGAATGAAC 2667
DB 438 TTGCAACCCCGCTGAGGCGCATTTCTATTATTCAGAGTTGTTTATCTTTGGAATGAAC 497
QY 2668 CGGCTGAGGCGCATTTCTGAAGAGATGATGATATGATATGCAATGTTGTTGCTAG 2727
DB 498 CGGCTGAGGCGCATTTCTGAAGAGATGATGATATGATATGCAATGTTGTTGCTAG 557
QY 2728 CAGAACCAAGTACCGGAGATATGCTATTCAGCTTGAAGCAATATGAAAGGTAAGTT 2787
DB 558 CAGAACCAAGTACCGGAGATATGCTATTCAGCTTGAAGCAATATGAAAGGTAAGTT 617
QY 2788 ATTAATGGATCGCTCAGAGATATTTTCATCATGCGGCCAAGAGAAAGAAATTCCTC 2847
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Db 486 TCGGTAGAGCCCATTCCTGAAAGATCGATGATGATATGCAATGTTGTTGCTAG 545
Qy 2127 CCAGAACCAATCACGGGCAATATGCTATTTGAGCTTGACCAATATGAAAGTAATT 2786
Db 546 CCAGAACCAATCACGGGCAATATGCTATTTGAGCTTGACCAATATGAAAGTAATT 605
Qy 2787 GATTAAATGGGATCGCTCAGAGATATTTATCATGCGGCGCAACAGAAAGAAATTTCC 2846
Db 606 GATTAAATGGGATCGCTCAGAGATATTTATCATGCGGCGCAACAGAAAGAAATTTCC 665
Qy 2847 CCAAGTTAACGACGCGCTTTCAGAGATTCGAAGTATCGGTTGGAATGAT 2901
Db 666 CCAAGTTAACGACGCGCTTTCAGAGATTCGAAGTATCGGTTGGAATGAT 720

RESULT 12
US-10-369-493-38964
; Sequence 38964, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38964
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38964

Query Match 22.4%; Score 711.8; DB 16; Length 720;
Best Local Similarity 99.7%; Pred. No. 1.9e-121;
Matches 713; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2187 CCTGATCTAATTTTCGGTCCAACTTGCAACAGAAAGCAACGACCGGATAGCTCTTGC 2246
Db 6 CCTGATCTAATTTTCGGTCCAACTTGCAACAGAAAGCAACGACCGGATAGCTCTTGC 65
Qy 2247 CCAGCAGACGAGGCTTCCAGTCCCTTGGCTGATCGGGTCCAAATCGTGTCTCAACTATC 2306
Db 66 CCAGCAGACGAGGCTTCCAGTCCCTTGGCTGATCGGGTCCAAATCGTGTCTCAACTATC 125
Qy 2307 AACCGGAAGCGGACGACCAACAGTGAAGAACTGAAGAAAGCAACGCTCTCACTTGA 2366
Db 126 AACCGGAAGCGGACGACCAACAGTGAAGAACTGAAGAAAGCAACGCTCTCACTTGA 185
Qy 2367 TGATCGGCTCTGTTGAGAGGTATATGCAACGCAAGTATCATTAAGGCTGATGCA 2426
Db 186 TGATCGGCTCTGTTGAGAGGTATATGCAACGCAAGTATCATTAAGGCTGATGCA 245
Qy 2427 GAGAGTATATATCATGAGGCGCAACGAGGCGCTTATTTCTGAGGAGAGATCAACTGTT 2486
Db 246 GAGAGTATATATCATGAGGCGCAACGAGGCGCTTATTTCTGAGGAGAGATCAACTGTT 305
Qy 2487 GCTCAACTGATGCGCGCAAAACAGCTATTTGAGTGAAGTCAATTTTCTTGGAATATATCG 2546
Db 306 GCTCAACTGATGCGCGCAAAACAGCTATTTGAGTGAAGTCAATTTTCTTGGAATATATCG 365
Qy 2547 CCAACAAGTTACCCGCAACAGAGACCTTATGAAAGCGGCAAGGCAAGTTAAGCAAT 2606
Db 366 CCAACAAGTTACCCGCAACAGAGACCTTATGAAAGCGGCAAGGCAAGTTAAGCAAT 425
Qy 2607 GTTGACACCCGCTGAGGCGCAATTCATATATTCAGAGTTGTTATCTTGGAATGAACG 2666

Db 426 GTTACACCCCGCTGACAGCCATTCATATATTCAGAGTTGTTATCTTTGGAATGAAC 485
Qy 2667 TCGGCTAGAGCCCATTCCTGAAAGATCGATGATGATATGCAATGTTGTTGCTAG 2726
Db 486 TCGGCTAGAGCCCATTCCTGAAAGATCGATGATGATATGCAATGTTGTTGCTAG 545
Qy 2727 CCAGAACCAATCACGGGCAATATGCTATTTGAGCTTGACCAATATGAAAGTAATT 2786
Db 546 CCAGAACCAATCACGGGCAATATGCTATTTGAGCTTGACCAATATGAAAGTAATT 605
Qy 2787 GATTAAATGGGATCGCTCAGAGATATTTATCATGCGGCGCAACAGAAAGAAATTTCC 2846
Db 606 GATTAAATGGGATCGCTCAGAGATATTTATCATGCGGCGCAACAGAAAGAAATTTCC 665
Qy 2847 CCAAGTTAACGACGCGCTTTCAGAGATTCGAAGTATCGGTTGGAATGAT 2901
Db 666 CCAAGTTAACGACGCGCTTTCAGAGATTCGAAGTATCGGTTGGAATGAT 720

RESULT 13
US-10-369-493-38966
; Sequence 38966, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38966
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38966

Query Match 22.4%; Score 711.8; DB 16; Length 720;
Best Local Similarity 99.7%; Pred. No. 1.9e-121;
Matches 713; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2187 CCTGATCTAATTTTCGGTCCAACTTGCAACAGAAAGCAACGACCGGATAGCTCTTGC 2246
Db 6 CCTGATCTAATTTTCGGTCCAACTTGCAACAGAAAGCAACGACCGGATAGCTCTTGC 65
Qy 2247 CCAGCAGACGAGGCTTCCAGTCCCTTGGCTGATCGGGTCCAAATCGTGTCTCAACTATC 2306
Db 66 CCAGCAGACGAGGCTTCCAGTCCCTTGGCTGATCGGGTCCAAATCGTGTCTCAACTATC 125
Qy 2307 AACCGGAAGCGGACGACCAACAGTGAAGAACTGAAGAAAGCAACGCTCTCACTTGA 2366
Db 126 AACCGGAAGCGGACGACCAACAGTGAAGAACTGAAGAAAGCAACGCTCTCACTTGA 185
Qy 2367 TGATCGGCTCTGTTGAGAGGTATATGCAACGCAAGTATCATTAAGGCTGATGCA 2426
Db 186 TGATCGGCTCTGTTGAGAGGTATATGCAACGCAAGTATCATTAAGGCTGATGCA 245
Qy 2427 GAGAGTATATATCATGAGGCGCAACGAGGCGCTTATTTCTGAGGAGAGATCAACTGTT 2486
Db 246 GAGAGTATATATCATGAGGCGCAACGAGGCGCTTATTTCTGAGGAGAGATCAACTGTT 305
Qy 2487 GCTCAACTGATGCGCGCAAAACAGCTATTTGAGTGAAGTCAATTTTCTTGGAATATATCG 2546
Db 306 GCTCAACTGATGCGCGCAAAACAGCTATTTGAGTGAAGTCAATTTTCTTGGAATATATCG 365
Qy 2547 CCAACAAGTTACCCGCAACAGAGACCTTATGAAAGCGGCAAGGCAAGTTAAGCAAT 2606


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QY 2428 GAGGTGTATATCATGAGGCCAACGGGCGGCTTATCTTGAGGAGGATCCACTCGTGG 2487
Db 247 GAGGTGTATATATATGAGGCCAACGGGCGGCTTATCTTGAGGAGGATCCACTCGTGG 306
QY 2488 CTCAACTGCATGCGCGGAAACAGCTATTTGGAGTGCAGATTTTGTGGCATTTATTTCGC 2547
Db 307 CTCAACTGCATGCGCGGAAACAGCTATTTGGAGTGCAGATTTTGTGGCATTTATTTCGC 366
QY 2548 CACAACTTACCCGACCAAGAGACCTTCATGAAAAGCGCCAGAGCCAGAGTTAAGCAGATG 2607
Db 367 CACGAGTTAGCAGACGACAGAGACCTTCATGAACTGGCCAGAGCCAGAGTTAAGCAGATG 426
QY 2608 TTGCACCCGCGTGCAGAGCCATTCCTATTTCAAGAGTGGTTTATCTTTGGAATGACCT 2667
Db 427 TTACGCCCTGCTGCAGAGCCCTTCTTATTTCAAGAGTGGTTTATCTTTGGAATGACCT 486
QY 2668 CGGCTGAGGCCCATTTCTGAAAGAGATCGATGATATCGAATATGCCATGTTGTTGCTAGC 2727
Db 487 CGGCTGAGGCCCATTTCTGAAAGAGATCGATGATATCGAATATGCCATGTTGTTGCTAGC 546
QY 2728 CAGAACCCAGATCACGGCAGATATGCTATTGACGCTTGACGCAATATGGAAGGTAAAGTTG 2787
Db 547 CAGAACCCAGATCACATCCGATATGCTATTGACGCTTGACGCAATATGGAAGGTAAAGTTG 606
QY 2788 ATTAAATGGGATGCTTCAGAGATTTTCATCCATGGCGCCAACAGGAAACAGAAATTCGCC 2847
Db 607 ATTCAATGGGATGCTTCAGAGATTTTCATCCATGGCGCCAACAGGAAACAGAAATTCGCC 666
QY 2848 CAAAGTTAACGACCGGCTTTCAGCGGATTCGAAGTCAATCCGTCGGAATGTAT 2901
Db 667 CGAGTTAACGACCGGCTTTCAGCGGATTCGAAGTCAATCCGTCGGAATGTAT 720
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Search completed: June 10, 2004, 14:22:30
Job time : 5037 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 9, 2004, 22:11:24 ; Search time 11837 Seconds

(without alignments)
8030.018 Million cell updates/sec

Title: US-10-072-077a-1

Perfect score: 3183

Sequence: 1 gatattctttttatctca.....tatgttactagatcgaatc 3183

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hrc:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	230.2	7.9	594 29	CG408874 Ds568 Ds
2	237.8	7.5	241 28	BZ382321 SALK_1181
3	216.2	6.8	628 14	CB860800 HH05G12w
4	216.2	6.8	636 14	CB861695 HH02106w

Result	Score	Query Match Length	ID	Description
5	210	6.6	286 28	BH854067
6	168.6	5.3	311 12	CF307942
7	168	5.3	584 14	B1807352
8	155.8	4.9	547 14	CF308453
9	150.4	4.7	284 14	CK295792
10	150	4.7	688 12	B1807349
11	137.4	4.3	222 14	CF308452
12	130	4.1	130 28	BH854062
13	121	3.6	1391 29	CG754863
14	113.6	3.6	1201 9	AL565455
15	113.6	3.6	1896 29	CG753083
16	107.6	3.4	1101 29	CNS00EVL
17	105.4	3.3	1200 13	BX415878
18	103.2	3.2	1201 9	AL565455
19	102.4	3.2	1201 29	CNS0167M
20	100.8	3.2	800 28	BH482052
21	99.2	3.1	1592 29	CG750135
22	98.8	3.1	1200 13	BX415878
23	98.8	3.1	1348 29	CG749499
24	98	3.1	405 28	BH618228
25	98	3.1	1200 13	BX437758
26	96.2	3.0	1101 29	CNS00EVL
27	95.8	3.0	1200 13	BX437758
28	95.8	3.0	1896 29	CG753083
29	92	2.9	1101 29	CNS00EVL
30	91.8	2.9	1210 29	CG749728
31	91.8	2.9	1310 29	CG749728
32	90.6	2.8	1101 29	CNS00EVL
33	90.6	2.8	1626 14	CF238805
34	89.4	2.8	1101 29	CNS00EVL
35	88.4	2.8	548 28	CC055940
36	87.8	2.8	1201 13	BX336467
37	87.2	2.7	1592 29	CG750135
38	87	2.7	1201 13	BX439779
39	86.4	2.7	1201 13	BX439779
40	86.2	2.7	1061 13	BX437039
41	86.2	2.7	1277 28	CC253231
42	86.2	2.7	1364 29	CG757970
43	86	2.7	1201 9	AL536104
44	85.8	2.7	1056 13	BX415058
45	85.8	2.7	1101 29	CNS0039G

ALIGNMENTS

RESULT 1
CG408874 594 bp DNA linear GSS 03-SEP-2003
LOCUS
DEFINITION Ds568 Ds insertion lines Oryza sativa (japonica cultivar-group)
ACCESSION CG408874
VERSION GI:34430239
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharitoidae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 594)
Kim C.M., Piao H.T., Park S.J., Chon N.S., Je B.I., Sun B.,
Park S.H., Park J.Y., Lee E.J., Kim M.J., Lee J.O., Nam M.H.,
Bun M.Y. and Han C.D.
Rapid, large-scale generation of Ds transposon lines and analysis
of Ds loci in rice
Unpublished (2003)
Contact: Chang-deok Han
Division of Applied Life Science, PwBRC
Gyeongsang National University
Gazwa-dong 900, Jinju 660-701, South Korea
Tel: +82 55 751 6029
Fax: +82 55 759 9363
Email: cdhan@nongae.gnu.ac.kr

Location: chromosome 3 clone OSUNB0020011
Class: transposon-tagged.

FEATURES

Location/Qualifiers
1..594
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Dongjin"
/db_xref="taxon:39947"
/clone_lib="Ds insertion lines"

ORIGIN

Query Match 7.9%; Score 250.2; DB 29; Length 594;
Best Local Similarity 98.8%; Pred. No. 1.5e-35;
Matches 252; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2925 GATGCTCAACATTTGGCAATTAAGTTCTTAAGATTGAATCCGTGGCGGCTTGGC 2384
DB 210 GATGCTCAACATTTGGCAATTAAGTTCTTAAGATTGAATCCGTGGCGGCTTGGC 269
QY 2985 ATGATTTCATTAATTTCTGTGAATTAGATTAGATGATTAATTAATTAATGATGC 3044
DB 270 ATGATTTCATTAATTTCTGTGAATTAGATTAGATGATTAATTAATTAATGATGC 329
QY 3045 ATGACGTTATTAAGATGAGTGGTTTATGATTAGATCCGCAATTATACATTATAC 3104
DB 330 ATGACGTTATTAAGATGAGTGGTTTATGATTAGATCCGCAATTATACATTATAC 389
QY 3105 GCGATGAAAAAATAATATGCGCGCAACTGGGATTAATATGCGCGGCTGTCATCT 3164
DB 390 GCGATGAAAAAATAATATGCGCGCAACTGGGATTAATATGCGCGGCTGTCATCT 449
QY 3165 ATGTTACTAGATGA 3179
DB 450 ATGTTACTAGATGA 464

RESULT 2
BZ382321 241 bp DNA linear GSS 26-NOV-2002
LOCUS BZ382321
DEFINITION SALK_118148.40.60.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_118148.40.60.n, genomic
survey sequence.

ACCESSION BZ382321
VERSION BZ382321
KEYWORDS GSS.

SOURCE
ORGANISM Arabidopsis thaliana (thale cress)

REFERENCE
AUTHORS Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 241)

TITLE
JOURNAL Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadgil, C., Jeske, A., Karney, M., Kim, C.J., Parker, H., Prednis, L.,
Shim, P., Zimmermann, J., and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 538 6379
Email: ecker@salk.edu

COMMENT
This is single pass sequence recovered from the left border of
TDNA.

Class: TDNA tagged.

FEATURES
source Location/Qualifiers
1..241
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"

/clone="SALK_118148.40.60.n"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 7.5%; Score 237.8; DB 28; Length 241;
Best Local Similarity 99.2%; Pred. No. 3.8e-34;
Matches 239; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1285 GAACTTCATAGAGATTCAGATGATGAATGGTGGGAAACATGTAACAGGAAAC 1344
DB 1 GAACTTCATAGAGATTCAGATGATGAATGGTGGGAAACATGTAACAGGAAAC 60
QY 1345 TTTTACCAATGATGATGATTTTATCTCAAAAATACTAGGATATGATGATGATG 1404
DB 61 TTTTACCAATGATGATGATTTTATCTCAAAAATACTAGGATATGATGATGATG 120
QY 1405 TTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1464
DB 121 TTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 1465 TTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1524
DB 181 TTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
QY 1525 T 1525
DB 241 T 241

RESULT 3
CB860800/c 628 bp mRNA linear EST 22-APR-2003
LOCUS CB860800
DEFINITION HH05G12w HH Hordeum vulgare cDNA clone HH05G12-5-PRIME, mRNA
sequence.

ACCESSION CB860800
VERSION CB860800.1 GI:30055359
KEYWORDS EST.

SOURCE
ORGANISM Hordeum vulgare

REFERENCE
AUTHORS Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 628)

TITLE
JOURNAL Varshney, R.K., Zhang, H., Burton, R., Stein, N., Langridge, P., and
Graner, A.
Barley ESTs from coleoptile tissue
Unpublished (2003)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 628 Std Error: 0.00
Plate: 5 row: G column: 12
Seq primer: T7.

FEATURES
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1..628
/organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Sloop"
/db_xref="GABI:535262"
/db_xref="taxon:4513"
/clone="HH05G12"
/issue_type="coleoptile"
/dev_stage="coleoptile, 1 day old"

/lab host="DH10B"
/clone_lib="HH"
/note="Vector: pSPORT; Site 1: SalI (5-end of cDNA);
Site 2: NotI (3-end of cDNA); Due to the cloning system
used blue/white selection for recombinants is not 100 %
reliable. Average insert size is 1.3 kb."

ORIGIN

Query Match 6.8%; Score 216.2; DB 14; Length 628;
Best Local Similarity 97.7%; Pred. No. 3.2e-30;
Matches 251; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 2922 CTCGATGCTTCAACATTTGGCAATTAAGTTCTTAAGATTGAATCCGTTGCCGCTT 2981
DB 264 CCCGATGCTTCAACATTTGGCAATTAAGTTCTTAAGATTGAATCCGTTGCCGCTT 206
QY 2982 GCGATGATTCATATTAATTTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTA 3041
DB 205 GCGATGATTCATATTAATTTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTA 146
QY 3042 TGCAATGATTCATATTAATTTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTA 3101
DB 145 TGCAATGATTCATATTAATTTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTA 87
QY 3102 TACCGGATGAGAAACAAATATGCGCGCAACTGGGATTAATTAATGCGCGCGGTGCA 3161
DB 86 TACCGGATGAGAAACAAATATGCGCGCAACTGGGATTAATTAATGCGCGCGGTGCA 28
QY 3162 TCTATGTTACTAGATCG 3178
DB 27 TCTATGTTACTAGATCG 11

RESULT 4
CB861695/c 636 bp mRNA linear EST 22-APR-2003
LOCUS HH02106w HH Hordeum vulgare cDNA clone HH02106 5-PRIME, mRNA
DEFINITION
sequence.
ACCESSION CB861695
VERSION CB861695.1 GI:30056254
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 636)
Varshney, R.K., Zhang, H., Burton, R., Stein, N., Langridge, P. and
Granel, A.
AUTHORS
TITLE Barley ESTs from coleoptile tissue
JOURNAL Unpublished (2003)
COMMENT Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 636 Std Error: 0.00
Plate: 2 row: 1 column: 6
Seq primer: T7.

FEATURES
Source

1..636 Location/Qualifiers
/organism="Hordeum vulgare"
/mol_type="mRNA"
/catalytic="Sloop"
/db_xref="GABI:534665"
/db_xref="taxon:4513"
/clone="HH02106"
/issue_type="coleoptile"
/dev_stage="coleoptile, 1 day old"
/lab_host="DH10B"
/clone_lib="HH"

/note="Vector: pSPORT; Site 1: SalI (5-end of cDNA);
Site 2: NotI (3-end of cDNA); Due to the cloning system
used blue/white selection for recombinants is not 100 %
reliable. Average insert size is 1.3 kb."

ORIGIN

Query Match 6.8%; Score 216.2; DB 14; Length 636;
Best Local Similarity 97.7%; Pred. No. 3.2e-30;
Matches 251; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 2922 CTCGATGCTTCAACATTTGGCAATTAAGTTCTTAAGATTGAATCCGTTGCCGCTT 2981
DB 260 CCCGATGCTTCAACATTTGGCAATTAAGTTCTTAAGATTGAATCCGTTGCCGCTT 202
QY 2982 GCGATGATTCATATTAATTTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTA 3041
DB 201 GCGATGATTCATATTAATTTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTA 142
QY 3042 TGCAATGATTCATATTAATTTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTA 3101
DB 141 TGC-TGACGTTATTAATTAAGTTGCGTTTATTAAGTTAGAGTCCGCAATTATTAATTAACATGTA 83
QY 3102 TACCGGATGAGAAACAAATATGCGCGCAACTGGGATTAATTAATGCGCGCGGTGCA 3161
DB 82 TACCGGATGAGAAACAAATATTAAGTTAGAGTCCGCAATTATTAATTAACATGTA 24
QY 3162 TCTATGTTACTAGATCG 3178
DB 23 TCTATGTTACTAGATCG 7

RESULT 5
BH854067 286 bp DNA linear GSS 13-JUN-2002
LOCUS BH854067
DEFINITION
SAIK 078693.24.40.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SAIK_078693.24.40.x, genomic
survey sequence.
ACCESSION BH854067
VERSION BH854067.1 GI:21424938
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 286)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadriah, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shim, P., Zimmerman, J. and Ecker, J.R.
AUTHORS
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.

FEATURES
Source

1..286 Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SAIK_078693.24.40.x"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/ldna_protocols.html

ORIGIN

Query Match 6.6%; Score 210; DB 28; Length 286;

Best Local Similarity 85.7%; Pred. No. 5.5e-29;

Matches 245; Conservative 0; Mismatches 40; Indels 1; Gaps 1;

1140 GTTACACTTCCAGCAATATGATTTGGATTAGTCCAAATGCAATTTGTAAGTATC 1199

1 GTTATCACTTACGCAATATGATTTGGATTAGTCCAAATGCAATTTGTAAGTATC 60

1200 CCTCTTGTCTTATGATTTATTTCAATTTCTTATTTATTTCCCTTATCTACAGAGC-TA 1258

61 CCTGTGCGCATATGATTTATTTCAATTTCTTATTTATTTCCCTTATCTGCGAGGCTA 120

1259 CATTATATTTGATTTCTATGACAGGGAACCTTTGATGACATTTGATGATTAATG 1318

121 CCTTATATTTGATTTCTATGACAGGGAACCTTTGATGATTTGATGATTAATG 180

1319 GTGGGAACATCATGATGACAGGGAACCTTTGATGATTTGATGATTAATGATTA 1378

181 GTGGGAACATCATGATGACAGGGAACCTTTGATGATTTGATGATTAATGATTA 240

1379 ATACTTACCGTATGATGATTTGATGATTTGATGATTTGATGATTTGATGATTTG 1424

241 ATACTTACCGTATGATGATTTGATGATTTGATGATTTGATGATTTGATGATTTG 286

RESULT 6

CE307942 311 bp mRNA linear EST 15-AUG-2003

LOCUS ABF--01-J01.b1 ABF3-overexpressing transgenic rice plasmid cDNA

DEFINITION 1:library (ABF) Oryza sativa cDNA clone ABF--01-J01, mRNA sequence.

ACCESSION CE307942

VERSION CE307942.1 GI:33679703

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 311)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Query Match 5.3%; Score 168.6; DB 14; Length 311;

Best Local Similarity 89.6%; Pred. No. 2.8e-21;

Matches 180; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

2922 CTGATGCTTCAACATTTGGCAATTAAGTTCTTAAGATTGAATCTGTGGCGGCTT 2981

66 CCGATGCTTCAACATTTGGCAATTAAGTTCTTAAGATTGAATCTGTGGCGGCTT 125

2982 GCGATGCTTCAACATTTGGCAATTAAGTTCTTAAGATTGAATCTGTGGCGGCTT 3041

126 GCGATGCTTCAACATTTGGCAATTAAGTTCTTAAGATTGAATCTGTGGCGGCTT 185

3042 TGCATGCTTCAACATTTGGCAATTAAGTTCTTAAGATTGAATCTGTGGCGGCTT 3101

186 TGCATGCTTCAACATTTGGCAATTAAGTTCTTAAGATTGAATCTGTGGCGGCTT 245

3102 TACGCGATTAACAAACAAATA 3122

246 AAAAAAAAAAAAAAAAAAAAAA 266

RESULT 7

BI807352 584 bp mRNA linear EST 02-OCT-2001

LOCUS S104H12 Stem library from Oryza sativa (3-5 leaf stage) Oryza

DEFINITION BI807352

ACCESSION BI807352

VERSION BI807352.1 GI:15854556

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 584)

AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X.,

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K., and Lou,Y.C.

QY 3056 TATGAGATGGGTTTATGATTAGATCCCGCAATTATACATTTAATACGGGATAGAAA 3115
 DB 433 TATGAGATGGGTTTATGATTAGATCCCGCAATTATACATTTAATACGGGATAGAAA 492
 QY 3116 CAATAATGGCGCCCAACTGGGATTAAT 3144
 DB 493 ACAATATAGCGCCCAACTAGATTAAT 521

RESULT 8
 CF308453/c
 LOCUS
 DEFINITION ABF-02-E14-g1 ABF3-overexpressing transgenic rice plasmid cDNA
 ACCESSION CF308453
 VERSION CF308453
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Erihartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 547)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..547
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Naekdong"
 /db_xref="taxon:4530"
 /clone="ABF-02-E14"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

ORIGIN
 Query Match 4.9%; Score 155.8; DB 14; Length 547;
 Best Local Similarity 98.7%; Pred. No. 6e-19; Indels 0; Gaps 0;
 Matches 157; Conservative 0; Mismatches 2;

QY 2922 CTCGATCGTTCAACATTTGGCAATAAAGTTCTTAAGATGAATCCTGGCGGCTT 2981
 DB 174 CCGATCGTTCAACATTTGGCAATAAAGTTCTTAAGATGAATCCTGGCGGCTT 115
 QY 2982 GCGATGATTCATATATATTTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTAA 3041
 DB 114 GCGATGATTCATATATATTTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTAA 55
 QY 3042 TGCATGACGTTATTTATGAGATGGGTTTATGATTTGA 3080
 DB 54 TGCATGACGTTATTTATGAGATGGGTTTATGATTTAA 16

RESULT 9
 CK295792/c
 LOCUS
 CK295792 284 bp mRNA linear EST 15-DEC-2003

DEFINITION EST758506 Nicotiana benthamiana mixed tissue cDNA library,
 normalized, full-length Nicotiana benthamiana cDNA clone NEMCX34.3'
 end, mRNA sequence.
 ACCESSION CK295792
 VERSION CK295792
 KEYWORDS
 SOURCE
 ORGANISM
 Nicotiana benthamiana
 Nicotiana benthamiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Nicotiana.
 1 (bases 1 to 284)
 Buell,C.R., Hart,A., Zisemann,V., Karaymicheva,S.A., Day,B.,
 Staskiewicz,B., Jin,H. and Baker,B.
 Generation of EST sequences from Nicotiana benthamiana
 Unpublished (2003)
 CONTACT: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from TIGR via potato@tigr.org
 Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
 Location/Qualifiers
 1..284
 /organism="Nicotiana benthamiana"
 /mol_type="mRNA"
 /db_xref="taxon:4100"
 /clone="NEMCX34"
 /tissue_type="abiotic and biotic stress-treated leaves,
 callus tissue and root tissue"
 /lab_host="DH10B-TONA"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA
 library, normalized, full-length"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: RNA was isolated from Nicotiana benthamiana
 tissues that include callus, roots from liquid culture
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
 challenged leaves (Pseudomonas syringae pv tomato 12 hr;
 Xanthomonas campestris pv campestris 12 hr, 18hr;
 Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
 campestris pv vesicatoria 18hr). RNA was isolated from
 these tissues and pooled in approximately equal molar
 amounts."

ORIGIN
 Query Match 4.7%; Score 150.4; DB 14; Length 284;
 Best Local Similarity 99.3%; Pred. No. 7.1e-18;
 Matches 151; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2922 CTCGATCGTTCAACATTTGGCAATAAAGTTCTTAAGATGAATCCTGGCGGCTT 2981
 DB 152 CTCGATCGTTCAACATTTGGCAATAAAGTTCTTAAGATGAATCCTGGCGGCTT 93
 QY 2982 GCGATGATTCATATATATTTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTAA 3041
 DB 92 GCGATGATTCATATATATTTCTGTTGAATTAAGTTAAGCATGTAATTAATTAACATGTAA 33
 QY 3042 TGCATGACGTTATTTATGAGATGGGTTTAT 3073
 DB 32 TGCATGACGTTATTTATGAGATGGGTTTAT 1

RESULT 10
 BI807349/c
 LOCUS
 DEFINITION BI807349 688 bp mRNA linear EST 02-OCT-2001
 S104G12 Stem library from Oryza sativa (3-5 leaf stage) Oryza
 sativa cDNA clone S104G12, mRNA sequence.
 ACCESSION BI807349
 VERSION BI807349
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Oryza sativa

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 688)
Dong, H. T., Li, D. B., Zhang, X. F., Dai, C. G., Sun, L. X., Pei, Y. X., Wu, H. F., Jiang, Y. X., Yu, F. C., Gao, Q. K. and Lou, Y. C.
A Gene Expression Screen in *Oryza sativa*
Unpublished (2001)
Contact: Haitao Dong, Dehao Li
Bioinformatics and Gene Network Research Group
Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P. R. China
Tel: 0086-571-86892051
Fax: 0086-571-86891525
Email: webmaster@esarray.org, URL: <http://www.esarray.org>
Seq primer: M13 forward primer.
Location/Qualifiers
1..688
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/clone="SI104G12"
/tissue_type="Stem"
/dev_stage="3-5 leaf stage"
/clone_id="Stem library from Oryza sativa (3-5 leaf stage)"
/note="Vector: pSport2"

ORIGIN

Query Match: 4.7%; Score 150; DB 12; Length 688;
Best Local Similarity 93.8%; Pred. No. 6.8e-18;
Matches 167; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

Oy 2368 CTGTTGCGGGCTTGGCGATGATTCATATATATTTCTGTGAATACGTTAAGCATGAA 3027
Db 623 CCGGTGGGGCTCGCCGATGATTCATATATTTCTGTGAATACGTTAAGCATGAA 564
Oy 3028 TAATTACATGTAATGCATGACGTTATTATGAGTGGGTTTATGATTAAGTCCGC 3087
Db 563 TAAATTAACATGTAATGCATGACGTTATTATGAGTGGGTTTATGATTAAGTCCGC- 505
Oy 3088 AATATATCATTATTAAGCGGATAGAAACAAATATGCGCGCGCAACAGGATTAAT 3145
Db 504 AATTATACATTATTAATCCGCGATAGAAACAAATATTAAGCGCGCAACATGAGTAAAT 447

RESULT 11
CF308452 222 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION ABF-02-B14.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--02-B14, mRNA sequence.
ACCESSION CF308452
VERSION
KEYWORDS
SOURCE
ORGANISM
ORIGIN

Oryza sativa
Oryza sativa
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 222)
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B. H.
Genomics and Genetics Institute, Greengene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6155
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..222

FEATURES
SOURCE

```

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF-02-E14"
/risue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/node=Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

```

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ORIGIN
Query Match      4.3%; Score 137.4; DB 14; Length 222;
Best Local Similarity 99.3%; Pred. No. 2e-15;
Matches 138; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      2922  CTGCATGCTTCACAAACATTGGCAATAAGTTCTTCAAGATTGATCCTGTTGCCGGCTT 2981
Db      84      CCCGATCGTTCAACACATTGGCATATAAGTTCTTCAAGATTGATCCTGTTGCCGGCTT 143
Qy      2982  GCGATGATTATTCATATATTTCTGTTGAATTAAGCTTAAGCATGATATTAACATGTA 3041
Db      144  GCGATGATTATTCATATATTTCTGTTGAATTAAGCTTAAGCATGATATTAACATGTA 203
Qy      3042  TGCATGACGTTATTTATGCA 3060
Db      204  TGCATGACGTTATTTATGCA 222

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RESULT 12
LOCUS      BH854062                      130 bp      DNA      linear      GSS 13-JUN-2002
DEFINITION      SALK_078685.53.75.x Arabidopsis thaliana TDNA insertion lines
                Arabidopsis thaliana genomic clone SALK_078685.53.75.x, genomic
                survey sequence.
ACCESSION      BH854062
VERSION        BH854062.1
KEYWORDS       GSS.
SOURCE         Arabidopsis thaliana (thale cress)
ORGANISM       Arabidopsis thaliana
                Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1 (bases 1 to 130)
AUTHORS        Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R.,
                Gadrinab,C., Jeske,A., Karnes,M., Kim,C.U., Parker,H., Prednis,L.,
                Shinn,P., Zimmerman,J. and Ecker,J.R.
                A sequence-indexed library of insertion mutations in the
                Arabidopsis Genome
                Unpublished (2001)
COMMENT        Contact: Joseph R. Ecker
                Salk Institute Genomic Analysis Laboratory (SIGAL)
                The Salk Institute for Biological Studies
                10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                Tel: 858 453 4100 x1752
                Fax: 858 558 6379
                Email: ecker@salk.edu
                This is single pass sequence recovered from the left border of
                TDNA.
                Class: TDNA tagged.
                Location/Qualifiers
                    1..130
                        /organism="Arabidopsis thaliana"
                        /mol_type="genomic DNA"
                        /strain="Columbia 0"
                        /db_xref="taxon:3702"
                        /clone="SALK_078685.53.75.x"
                        /clone_lib="Arabidopsis thaliana TDNA insertion lines"

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RESULT 14	AL656545	1201 bp	mRNA	linear	EST 12-MAY-2003
LOCUS	AL656545				
DEFINITION	AL656545 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone				
ACCESSION	CS04DF005Y018.3-PRIME				
VERSION	AL656545				
KEYWORDS	AL656545.2 GI:30549492				
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1. (bases 1 to 1201)				
AUTHORS	Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	On Feb 16, 2001 this sequence version replaced gi:112916848.				

FEATURES	Location/Qualifiers
SOURCE	1. .1201

ORIGIN

Query Match	3.6%;	Score 113.6;	DB 9;	Length 1201;
Best Local Similarity	35.6%;	Pred. No. 3.7e-11;		
Matches 315;	Conservative 134;	Mismatches 433;	Indels 2;	Gaps 2

QY	1009	AAGATCCAAAGATPAPGTTCTTACTCTTCCTTGTTGGTAAGAAAACATACTATATCACTATPA	1066
Dd	320	AATCCAAAAAACAATTCTTACTTCCCCTGTGGTAGGTGCCACGAATGGAAGASTPAAG	379
QY	1069	TAAATATATCTAACATCATATATATTTGTAATAATAGCAGTATATTTGCATATTTTGAATTG	1128
Dd	380	CATTAATAATGATATTCAGTGCAGATGGAAGAAGGATATATATCCATATAMATAMAT	439
QY	1129	TATTTAGCGGTATACCTTCAGCGCAAATATGATTTGSATTTTAAGTCCAAAATGCATTT	1188
Dd	440	AAAT	499
QY	1189	TCGTAGCATCCCTCTTGTCGTCTAATGATTATTTCAATATATTTCTTATATATATCCCTAAC	1248
Dd	500	AAATATATATATATAT-AMATA	558
QY	1249	TACGAGACTCATTTATATTTSTATTCTPATGACAGGGAACTTCATATAGAGTTCCAGATA	1308
Dd	559	TAAATA	618
QY	1309	GATCAAAATTTGGTGGAAACATCATTTGAAACAGGAAACTTTAGCCAATCATATCCGATTTAT	1368
Dd	619	TAAATATATATATATATATATAT-ATATATATATATATATATATATATATATATATATATAT	677

[illegible]

RESULT 15	
CG753083	
LOCUS	1896 bp DNA linear GSS 24-OCT-2003
DEFINITION	P048-I-C01.za Ppa EcoRI BAC library <i>Pristionchus pacificus</i> genomic/c.
ACCESSION	CG753083
VERSION	CG753083.1 GI:37977199
KEYWORDS	GSS.
SOURCE	<i>Pristionchus pacificus</i>
ORGANISM	<i>Pristionchus pacificus</i>
REFERENCE	1 (bases 1 to 1896)
AUTHORS	Srinivasan,J., Sim,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.
TITLE	An integrated physical and genetic map of the nematode <i>Pristionchus pacificus</i>
JOURNAL	Mol. Genet. Genomics 269 (5), 715-722 (2003)
MEDLINE	22835951
PUBMED	12884007
COMMENT	Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Fax: 00497071601498 Email: ralf.sommer@tuebingen.mpg.de Class: BAC ends.

/note="The library was generated by a partial digest of

the genomic DNA with *Ec*RI and cloning into the *BAC* vector."

Query Match	3.6%;	Score 113.6;	DB 29;	Length 1896;
Best Local Similarity	42.4%;	Pred. No. 3.3e-11;		
Matches 699;	Conservative	0;	Mismatches 939;	Indels 12;
				Gaps 7;

[illegible]

Db	1064	TAAATATAATATATATATATTTTAAATTAATAATAATANAATTTTATTTTAAATTTTAA	1123
OY	1161	GATTGGATTTAAGTCCAAAATGCAATTTGGACGTAACCTCTTGCGCTAATGATTA	1220
Db	1124	TATTAATATTTTATTAATATTAATTTTATTTTATTTATTAATTAATTAATAATTAATTT	1183
OY	1221	TTTCAATATTTCTATATTAATCCCTACTCAAGACGACACNTTAATGTAATCTANGA	1280
Db	1184	TTATTTAAATTAATTAATTTTATTAATAAATAATTAATTAATTAATTAATTTTATTAATA	1243
OY	1281	CAGGAAACCTTCCATGAGATTCCAGATAGATGCAATTTGGTGGAAACATCA---TTGAA	1336
Db	1244	TTTTTTTNNATNTATNTATNTATTAATAAATTTTTTTTTTTTATTTATTAATTTAAT	1303
OY	1337	CAGGAAACCTTTAGCAATCATATCGATTATCTCAAAAAGATCTTAAGGTAATGAAG	1396
Db	1304	TTAATTAATTTTAAAAAATATATATTTTATTAATTTTATNTATNTATTTTA-TATATATT	1362
OY	1397	TTCCCTGGTGGAGACATATGATTGACAAATAGTAAATTTTGTCGCAATCATTTTT	1456
Db	1363	TATATNTNNATATTTAAATATATTTTAAATATTTAAATAAATAATTTANNTATATTT	1422
OY	1457	CTTTTGATTTGATTAAGCTTTTACTGACGAGATGGTCTCTTGGAATTAACAGAAAT	1516
Db	1423	TTTTTTTATTTNNAAATTTTATTTATTAATAATATAATTTTANNTAAAAAATAAAAAA	1482
OY	1517	CTTTGAATTCAACTATTTGATTAGTGAAGAACAAGAAAGATTCTTGTTTTATGTG	1576
Db	1483	AAAATATATTTTANNTATATATTAATTTTAAATTAATAAATATTAATTAATTT	1542
OY	1577	ATTGAGATTTTGATGATGAAGAAGTACCTACGACACAGAAGAAATTAACAATGACGT	1636
Db	1543	AAAAATATAAAT-ATATAAAAAATATATATAATTAATTAATTAATNTATTTTAAATATAT	1601
OY	1637	AACACGATACAGCATGTAAAGATTTTTCGCAATAATTTATACGATGATGATTT	1696
Db	1602	TATTAATATATAAATTTNAAAAATATATTTTTTTTTTNNATATATAATTTATTTATTTTT	1661
OY	1697	TTTTTTTTGAATGTCATTAATAAATGCTTCTTAATAATTAATTTTAATTAATTAAT	1756
Db	1662	AATATATTTTATATAATAATTTTANATTTTATTTTATNTAATTAATTAATTAATTAATA	1721
OY	1757	AAGGAATATATTTATGCAAAACATATCA	1786
Db	1722	ATATTTATATATTTATTTAAATNTATTTA	1751

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Job time : 11847 secs